```
Qy       665 -----------------------------------------------LeuThrLeuGlnGlyLeuProGlu 672
                                                            |||       |||       |||
Db      5221 TTTTCTAATGCAAAATAATAGACTTTTTTTTACACGCATTTAGGATATAGTGGCACACCA--- 5277

Qy       673 GlyTyrSerTyrLeuVal---------------------------LysGluThrAspSerGluGly 685
                 |::|||||||||:::                                   |||
Db      5278 GGAGTTAACTATCTTCTCGTAATGTTTCTTTTTTAACGCCAAACCTCGGATAAGTCAAAA 5337

Qy       686 TyrLysValLysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyIle 705
                 ||||||     :::::|::|||
Db      5338 CTTGTCTACAAAAGTCACTCGCAAAACAAGTCACC------------------------- 5370

Qy       706 ThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyVal 725
                 |||                                  |||||||||
Db      5371 --------GAAAACTTCGTGGATGTGCAACGGTGCCAAAAATCACTGCACCAACAGGCTTC 5421

Qy       726 AspGln 727
                 |||
Db      5422 ACCCAA 5427
```

```
Best Local Similarity: 20.20%         Mismatches: 301
Query Match:           3.52%          Indels:     214
DB:                    10             Gaps:       39

US-09-494-297-2 (1-757) x US-09-070-927A-167 (1-19031)


Qy    5  ArgPheProAsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSerLys   24
         :::|||  |  |||                  |||
Db       AAGTTTACTAATTTTTTGTATCGTATAAAATGACTTTGATGTGAAAGGTAATAAC------ 3600

Qy   25  ArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSerMet   44
                          :::
Db 3601  --ATAGGTTATAAGACTGTGAGTAGCCCAATCTATTACCATCTG                   3642

Qy   45  ValGlyAlaLysThrValPheGlyLeuValLeuSerSerThrProAsnAlaIleAsnPro   64
         ||||||      :::
Db 3643  ACCAACCGCGGTGTCACCGAAAACTTCGTAGATACAAGTGGCGCCGCAAAATCACGCCACCA 3702

Qy   65  AspSerSerGluTyrArgTrpTyrTyrGlyTyrGluSerTyrValArgGlyHisProTyr   84
         |||||          :::
Db 3703  AGTAATTTCACCCAA----------GGGAAACAAACGGTCATTAACAGTGATCCTTAC---- 3750

Qy   85  TyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyr  104
         :::
Db 3751  ---------------------------------------------------ACGTTC     3756

Qy  105  GlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSer---SerVal  123
         |||||     :::|||||  :::
Db 3757  CAACAAAGTGGTTTT---TTACCCGAGACCTCAAAAGTTGCCACGAAAATTACCGATTC    3813

Qy  124  LysLysTrpTyrTyrLysTyrHisAspGlyIleSerThrLysLysPheGluAspTyrAlaMet 142
         ||||||||
Db 3814  AAAGGCTGGTTACAAAGGG-------AAAACCAAAACCGAGCCTTTGGCCACCACT    3861

Qy  143  -----SerProArgIleThrGlyAspGluLeuAsnGlyLysLeuArgGlnAlaValMet  159
            |||     |||      :::||||||
Db 3862  AAAACACCTAGCTATAAAAGTCACGTATGATGAC---AATGATGAATTTGACGGTGTCTAT 3918

Qy  160  -----TyrArgAsnGlyHis-----ProGlnAsnAlaAsn-----GlyIleMetGluGly 173
         :::
Db 3919  GAGGAGTTTTCAGGGTACAGGCTGCTTCGACCAATCAAATTGGCTTTGTGGAT---   3975

Qy  174  LeuGluProLeuAsnAlaIleLeuArgValThrGlnGluAlaValThrTrpTyrTyrSerAspAsn 193
                |||     :::
Db 3976  --GAAGCGACGAACAAAATTAATTGCCCCCGACCAAGTGCGAGATGGAGTAGTATAAT---   4026

Qy  194  AlaProIleSerAsnProAspGluSerPheLysArgGluSerGluSerAsnLeuValSer  213
                 :::||||||
Db 4027  --CTTACTTTAAATGAAAAAATAAATAAAAACAGTAATGACCAGTAACTTAACGGGGG   4080

Qy  214  ThrSerGlnLeuSerLeuMetArgGlnAlaIleLeuIleAspProAsnLeuAla       233
         |||
Db 4081  ACAGATACAGCGACACTG----------------------AAAAACTTGTCC          4110

Qy  234  ThrLysMetProLysGlyValProAspAspPheGlnLeuSerIlePhe---GluSerGlu 252
         :::|||
Db 4111  -----GTGCCGTCAACTATTTGAACAATATCCGGTCAATACGTTTTATGGCCGGAGT     4164

Qy  253  AspLysGlyAspLysTyrArgAsnLysGlyTyrGlnAsnLeuLeuSerGlyLeuValPro 272
         ||| :::
Db 4165  GACATTACGTTTACATTGCCCAAACGGTACAAAATCAAATCAATATT-------       4209

Qy  273  ThrLysProProThrProGlyAspProProMetPro--ProAsnGlnProGlnThrThr  291
         ||| |||      |||
Db 4210  ACCAAAATCAGATGGCAAAACCAGCCGTTTCCTCTTCCTAAAATCATAATATAGAT       4269

Qy  292  SerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGluGlyAlaThr    311
         |||    :::
Db 4270  CAAGTAGAAAATGTCACACATGCCCTGACCACTTATAACAAGTTG---------       4314

Qy  312  LeuGlnLeuThrGlyAspAsnValAsnSerPheGlnLeuArgValPheSerSerAsnAsp 331
         ||||||||:::|||
Db 4315  AAAACAGCTGTCGGGC------------CAAACGTTTGGCTTTAAATGCT          4350
```

```
Qy  332  IleGlyLeuArgIleGlyLeuSerAspGlyThrThrTyrThrLeuThrGluLeuAsnSerPro 351
         :::     :::
Db 4351  TTAGCCGATCAACCTGAATTT------------------TATACGAAAACGTTATTGGGACAGAG 4398

Qy  352  AlaGlyLysTyrSerIleAlaGluProIleThrPheLysTyrValGlnLeuAlaGlyLysValTyrThr 371
         ||||||      :::||||||
Db 4399  TCTGGC--------ATCGATGACCCAGTCAATTATTATTACAATGAGTGGCCCGTTTAC-- 4449

Qy  372  IleIleAspGlyLysGlnIleLeuGluGlyAsnProAsnLysGlyGluIleValGluProTyrSerVal 391
Db 4449  ---------------------------------------------------------- 4449

Qy  392  GluAlaTyrAsnAspPheGluGlyPheSerValLeuGlnAsnTyrAlaLysPhe        411
Db 4449  ---------------------------------------------------------- 4449

Qy  412  TyrTyrArgAlaLysAsnLysGlySerSerGlnValValThrTyrCysPheAsnAlaAspLeu 431
         ||||||      :::
Db 4450  TATTATTTAGAAAAAACCCGAAAGTCACCGAGAACTTCCGTAGACACCAACGGCCGCTAAAATC 4509

Qy  432  LysSerSerProProAspSerGluAsnGlyGlyValGlyLysTyrThr               450
         :::|||     :::|||
Db 4510  ACACCCGGCCAACAGGTTTCACCCAAGGTAAAAAAACGGTGATTACAAGGGAC-- 4560

Qy  451  GlyGluValLysTyrThrHisIleIleAlaGlyValArgAspLeuPheLysTyrThrValPro 470
         |||
Db 4561  ----------------------GCCTACACTTTCAAACAA                     4578

Qy  471  ArgAspThrAspProAspThrPheLeuGluLeuLysHisIleLeuGlyLysGlyTyrTyr  490
         ||| :::||||||
Db 4579  GCAGGCACCTTACCCAGACACTTACCAACAGCGGGTAAGACCTACAAGTTCAAAGGTTGG 4638

Qy  491  ArgGlyLysGlyGlnAlaIleAlaLeuGluTyrSerGlyLeuThrGlnIleLeuArgAlaAla 510
         ||| :::
Db 4639  ---TACAAAGGCAAGTCCATA--CTCAACACATTGACAACTACC----           4686

Qy  511  ThrGlnLeuLeuAlaIleGluTyrTyrPheThrHisAspSerAlaGluLeu--AspLysAspLys 528
         |||
Db 4687  AGTTATCAAGTGACCTACGACACAATGAGTGGGTGTGATGAAGAGAAACA         4746

Qy  529  LeuLysAspAlaTyrHisGlyIlePheGlyAspMetAsn                       541
         :::|||
Db 4747  GTTTACGACAGTCGTATCCATCAGTCGATATGAATATTGAAAAAGGCGGGGCGGGGCTTTC 4806

Qy  542  ThrArgLeuAlaValAlaLysIleLeuLeuValGlyTyrArgAlaGlnIleAspPheSerAsnProGlnLeu 561
         |||
Db 4807  ACACCGCGGTTAACTTTAGTGGTAAGTACTATGCCGAAGATGCGACGTACTTAAGA    4866

Qy  562  ThrAspLeu----AspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThr 580
         ||||||||     :::
Db 4867  ACCGATTTTATGACCTGACCTCAAAAAATAATGGGCAACAAATAACGGTAAGTATT   4926

Qy  581  GlnTrpHisProGluAspLeu---ValAspIleIleLeuArgMetGluAspLysLysGluVal 599
         |||
Db 4927  AATAATCGTAGTATGCCATTTGTCCCAAGAATTATTGAAAAATATAATAAATGGACAACCA 4986

Qy  600  IleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuValAlaGlyAspArg 619
         ||| :::
Db 4987  ATCAGTGCTACCAACAGATTACAGTTT-----AATGTTGATAAAATTGCCATACGACCAA 5040

Qy  620  ThrLysAspPhePheHisPheGlyIleGluLeuLysAsnAsnLysGlyGluLeuLeuSer-- 638
         ||||||      |||
Db 5041  CAACTAAAATATTGTTGACAGATTCAAATTAGACACAGCTCAAAGTAGCAAACTTGAAAATCC 5100

Qy  639  ---GlnThrValLysThrAspLysThrAsnLeuGluPheLysAspAspLysAla------ 655
         :::     |||
Db 5101  TATAGATATGTTGTACACGAACAATAGCTCACTGGTTTTGTCGACCAAATGTACCACAGCA 5160

Qy  656  ------------------------ThrIleAsnLeuLysHisGlyGluSer----      664
         :::|||||      :::|||
Db 5161  GAGGTTGACCTTAGTTCAGAAATCTCTTAACTTGCTTAATTTTGATTCAGATGGCACCTAT 5220
```

```
Qy    368 LysValTyr------------------------Thrile----------------IleAspGlyLysGlnIleGlu 379
              |||                          :::
Db   5713 TTTAAAATATTTGCCCCAGCTAATACACTTGATGAAAAACCTAGAAGAGAAGCAATTGAT 5772

Qy    380 AsnProAsnLysGluIleValGluPro----------TyrSerValGluAlaTyrAsnAsp 396
              |||                          |||    :::
Db   5773 TTTACTGGAAAATTTAATTAATTGACGAAAATAATTTATTTGATGAATATAGAGGA 5832

Qy    397 PheGluGluPheSerValLeuThrThrGlnAsnThrTyrAlaLysPheThrTyrArgAla------ 414
Db   5833 GCTGTAGATAATGGAAAGAATTAGATGGTGAAATGCAA----TATTTTAGCCCAGAA 5883

Qy    415 ------LysAsnLysAsnSerSerGlnValValTyrCysPheAsnAla------ 429
Db   5884 ACAGGTAAAGCTTTTAAAGGTCTTAAAATCAAAATAGGTGATTAATAAAAACACTATTTTCAATTCT 5943

Qy    430 Asp----------LeuLysSerProProAspSerGluAspThrHisIleAlaGlyArg---------- 447
Db   5944 GATGGAGTTATTGCAAAAAGGATTTTGTAGTTAAGATGATAATAAAACACTATTTTGATGAT 6003

Qy    448 PheThrThrGlyGluValLysTyrThrHisIleGluLysGly------ 461
Db   6004 TCTGGTGTTATGAAAGTAGGTTACACTGAAATAGGCAAGCATTCTACTTTGCTGAA 6063

Qy    462 ------AspLeuPheThrTyrThrValLys 469
Db   6064 AACGGAGAAAATGCAAATAGGAGTATTTAATACAGAGATAGGATTTAAATAT 6114

Qy    470 ProArgAspThrAspProAspThrPheLeuLysHisIleLysValIleGluLysGly------ 489
Db   6115 TTTGGCTCATCATAATGACAGAGATTTA 6138

Qy    490 TyrArgGluLysGlyIleAlaIleLeuGlyThrTyrSerGlyLeuThrLeuThrGlnLeuArgAla 509
              |||::||:::|||  |||::::|||      ||||||||||:::
Db   6139 GGAAATGAAGAAGGTGAAGAAAATCTCATATTCTGGTATATAATAAATTCAATAATAAA-- 6195

Qy    510 AlaThrThrGlnIleLeuAlaIleGluTyrTyrPheThrArgAspSerAlaGlu---------- 523
              ||||||||||:|||||    |||
Db   6196 ATTTTACTATTTGATGATTCATTTTACAGCTGTAGTTGGATGGGAAA 6240

Qy    524 ------LeuAspLysAspSerAsnProGlnLeuThr 534
              |||::||:|||||    |||
Db   6241 GATTAGAGGATGGTTCAAAGTATTATTTATATAAAGAATAACAGCAGAAGCATAATATAGGT 6300

Qy    535 PheGlyAspMetAsn------------AspSerThrLeuAlaValAla 546
              :::||||              |||  |||
Db   6301 TTGTCATTAATAAAGTGTCAATATATTATTTTTAATGATGATGGAATTATGCAAGTTGGA 6360

Qy    547 LysIleLeuValGlu------------LysTyrGlnSerLeu 551
                  ::||||              |||
Db   6361 TTTGTCACTATAAATGATAAAAGTCTTCTCTACTTCTCTGAAATTATAGAAATCTGGA 6420

Qy    552 ------TyrAlaGlnAspSerAsnProGlnLeuThr 562
              |||:||:||||    |||
Db   6421 GTACAAACATAGATGACAATTATTTCTATATAGATAATGGTATATAGTTCAAATTGGT 6480

Qy    563 AspLeuAsp-----------PhePheIleProAsnAsnAsn------ 572
              :::||||           |||    |||
Db   6481 GTATTTGATACTTCAGATGCGATATAAAAATATTTTCCACCTGCTAATACTGTAAATGATAAT 6540

Qy    573 ------LysTyrGlnSerLeu 577
              |::|:||
Db   6541 ATTTACGGACAACCAGTTGAAATAATTAGTGGTTTTAGTTAGAGTTTGGGGAGAGATGTATATTAT 6600

Qy    578 ------IleGlyThrGlnTrpHisProGluAspLeuValAspPheIle 591
              |||::|||      ||||||
Db   6601 TTTCGGAGAAACAATATCAATTGCCTTAGAGTTTGGGGAGAGTTATATGGAA 6648

Qy    592 ArgMetGluAspGlyLysGluValIleLeuProValThrHisIleAsnLeuThrLeuArgLysThr 611
              |||||||              :::|||
Db   6649 AATGAAAGTAGATAAAACAATATACAATTGAGACTGGATGG 6693
```

```
Qy    612 ValThrGlyLeuAlaGlyAlaGlyAspArgThrLysAspPheHisPheGlu------ 626
              |||::|                   ::::|
Db   6694 TGCAAAGGTATTAATTAATTGATGATAAAAATATTATTTTTGATGAGAAGGCATAATG 6753

Qy    627 ------IleGluLeuLysAsnAsnLysGlnGluLeuSerGlnThrValLys 642
              :::|||||||
Db   6754 AGAACGGGGTCTTATATCATTTGAAAAATAATTATTATTTGAAT 6795

Qy    643 ThrAspLysThrAsnLeuGluGluPheLysAspGlyLysSerAlaThrIleAsnLeuLys------ 660
              |||  |||                          |||      |||
Db   6796 AATGAGAATGGTAGAAATGCAATTGGTATATAATAATAGAAGATAAGATGTTC 6795

Qy    661 ---HisGlyGluSerLeuThrLeuGln------------GlyLeuProGluGlyTyrSer 675
              |||||:||:||      |||::::|||
Db   6850 TATTTTGGTGAAGATGGTGTCATGCAGATTTAATAATACACCAGATGGAGATTTAAA 6909

Qy    676 TyrLeuValLysGlu 680
              :::
Db   6910 TACTTTGCACATCAA 6924
```

RESULT 15
US-09-070-927A-167
Sequence 167, Application US/09070927A
Patent No. US2002120116A1
GENERAL INFORMATION:
 APPLICANT: Charles A. Kunsch
  Steven Barash
  Patrick J. Dillon
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 982
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: Human Genome Sciences, Inc.
  STREET: 9410 Key West Avenue
  CITY: Rockville
  STATE: Maryland
  COUNTRY: USA
  ZIP: 20850
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
  COMPUTER: HP Vectra 486/33
  OPERATING SYSTEM: MSDOS version 6.2
  SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/070,927A
  FILING DATE: 04-May-2000
  CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 60/046,655
  FILING DATE: 1997-05-16
  APPLICATION NUMBER: 60/044,031
  FILING DATE: 1997-05-06
  APPLICATION NUMBER: 60/066,009
  FILING DATE: 1997-11-14
 ATTORNEY/AGENT INFORMATION:
  NAME: Kenley K. Hoover
  REGISTRATION NUMBER: 40,302
  REFERENCE/DOCKET NUMBER: PB369
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (301) 309-8504
  TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 167:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 19031 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-070-927A-167

Alignment Scores:

Pred. No.:	0.0322	Length:	19031
Score:	139.00	Matches:	158
Percent Similarity:	34.14%	Conservative:	109

RESULT 14
US-10-011-366-9

; Sequence 9, Application US/10011366
; Publication No. US20030054493A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
;   Kink, John A.
; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
;   OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
;   DISEASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Medlen & Carroll
;   STREET: 220 Montgomery Street, Suite 2200
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: United States of America
;   ZIP: 94104
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10,011,366
;   FILING DATE: 16-No.
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/957,310
;   FILING DATE: 23-OCT-1997
;   APPLICATION NUMBER: US 08/329,154
;   FILING DATE: 24-OCT-1994
;   APPLICATION NUMBER: US 08/161,907
;   FILING DATE: 02-DEC-1993
;   APPLICATION NUMBER: US 07/985,321
;   FILING DATE: 04-DEC-1992
;   APPLICATION NUMBER: US 07/429,791
;   FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ingolia, Diane E.
;   REGISTRATION NUMBER: 40,027
;   REFERENCE/DOCKET NUMBER: OPHD-01121
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 705-8410
;   TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 7101 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..7098
;   SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-011-366-9

Alignment Scores:
Pred. No.:   0.00756
Score: 139.00
Percent Similarity: 30.57%

Length: 7101
Matches: 154
Conservative: 86

Best Local Similarity: 19.62%
Query Match: 3.52%
DB: 14

Mismatches: 249
Indels: 296
Gaps: 38

US-09-494-297-2 (1-757) x US-10-011-366-9 (1-7101)

Qy   690 ------------------ValAsnSerGlnGluValAlaAsnAlaThrValSerLysThr 703
                            ||||| ||| :: :::
Db   3292 AAAGCCTTGACTATGTGGTGGAATGGCAAAGCGCGAGTTGACTGGGGTGATCGAACGGCTAT 3351

Qy   704 GlyIleThrSerAspGluThrLeuAlaPheGluAsnAsn 716
          |||||||| :::||| ||||:||::
Db   3352 CAAATCACTAAAGATAAAAGACAGCTTGATTGAAAACAAC 3390

Qy   690 ------------ValAsnSerGlnGluValAlaAsnAlaThrValSerLysThr 703
                        ||||| :|| ::: :::
Db   3232 GATAAAAAGGGGATCGGCATCAAATACAACCACCATATCACTATCACTCAAATCCCTAA 3291

Qy   93 --------------------AspLeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyr 107
                               :::: ||||||::: |||
Db   4897 CCATATTTCATTAGTTAATACACTAGAAACTAATTATATTTATATGTAGGAAATAGA 4956

Qy   83 ProGlyTyrTyrLysGlnPheArgValAlaHis------------------------- 92
          ||||:|| ::: :::||||:: ::||| |||
Db   4957 CAAAATATGATAGTGGAACCAAATTATGATTTAGATGATTCTGAAGATATATCTTCACT 5016

Qy   128 LysLysHisAspGlyIleSerThrLysPheGluAspTyrAlaAlaMetSerProArgIleThr 147
                                ::: |||||::: ||||||:::
Db   5017 GTTATCAATTTCTCTCAAAAGTATCTTTATGGAATAGACAGTTGTTAATAAA----- 5070

Qy   108 CysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerValLysTrpIleTyr 127
          |||||||||::::::|||
Db   5095 ACAGATGAAATAAAAATAATACGCCCTGTATATGAACACAAAAATAATACTTATCTTATT 5154

Qy   148 GlyAspGluLeuAsnGlnLysLeuArgGlyAlaValMetTyrAsnGlyHisProGln------ 165
          ||||::: :::::||||
Db   5155 GTATTAGATGCAAATAATATAATAAAATGAAAAATAAAT-- 5211

Qy   166 ------AsnAlaAsnGlyIleMetGlyGlyLeuGluProLeuAsnAlaAlaIleArgValThr 183
                     ::: ||| ||| ||| |||
Db   5212 ATACGATATGTATCG---------------------AGTAATAAGATGGTAATGATTTTT 5247

Qy   184 GlnGluAlaLeuTrpIleTyrTyrSerAspProAsnAlaProIleSerAspAsnProGluSerPhe 203
                            ::::||||||:||
Db   5155 GTATTAGATGCAAATAATATAATAAAATGAAAAATAAAT 5211

Qy   204 LysArgGluSerGluAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAla 223
          ::: ||||||||||||||::: |||
Db   5248 ATTCTTATGTCAACTAGTGAAGAAAATAAGGTGTCACAACTT 5289

Qy   224 LeuLysGlnLeuIle--------------AspProAsnLeuAlaThrLysMetProLysGln 239
                                         ||| ||| |||
Db   5290 AAAATAAGATTCGTTAATGTTTTTAAAGATAAAGACTTTGGCAAATAAAGGCTATCT---- 5343

Qy   268 Gly----------GlyLeuValProThrLysProGlyProThrProGlyAspProProMetPro 284
          ||| ||||||
Db   5377 AGTGAAAATAAATCTTATCATTTACACCTTCATAT------TATGAGGATGGAATTGATT 5427

Qy   257 -----------------LysTyrAsnLysGlyTyrGlnAsnLeuLeuSer 267
                            ::::|||
Db   5344 TTAACTTTAGTGATAAAGAACAAGATGTACCTGTA--------- 5376

Qy   240 ValProAspAspPheGlnLeuSerIlePheGluSerGluLysGlyLysAsp--------- 256
                    :|||||||||||
Db   5344 TTAACTTTAGTGATAAAGAACAAGATGTACCTGTA--------- 5376

Qy   285 ProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSer 304
          |||::: :::|||
Db   5428 GGCTATGATTGGGTCTAGTT--------------------- 5448

Qy   305 LysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAla 324
                    ||| ||| :::
Db   5488 ATGATGGGTATCTGA----- 5541

Qy   325 ArgValPheSerArgAsnAspIleGlyIleuArgIleGluLeuSerAspGlyThrTyrThr 344
          ||| :||| ::::::
Db   5542 CCAGTA----AATAATTTGATAACTGGATTTCGTGACTGGTAGGCGATGAATAAATACTAC 5595

Qy   345 LeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIle------------ 360
                     ::: |||||||||
Db   5596 TTTAATCCAATTAATGGTGGAGCTGCT--TCAATTGGAGAGACAAATAATTGATGACAAA 5652

Qy   361 ----------ThrPheLysValGluAlaGly 367
                    ||| |||
Db   5653 AATTATTATTTCAACCAAAGTGGAGTGTTACAAACAGGTGTATTAGTTAGACAGAGATGGA 5712

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; LOCATION: (1)...(3504)
US-09-815-242-7425

Alignment Scores:
Pred. No.:
Score:                    0.00239        139.50
Percent Similarity:       34.50%                  Length:         3504
Best Local Similarity:    19.07%                  Matches:        136
Query Match:              3.54%                   Conservative:   110
DB:                                      9        Mismatches:     282
                                                  Indels:         185
                                                  Gaps:           32

US-09-494-297-2 (1-757) x US-09-815-242-7425 (1-3504)

Qy   103 SerTyrGlnValTyrCysPheAsnLeuLeuLysLysAlaPheProLeuGlySerAspSerSer   122
             ::    :::
Db  1510 TCTTATTATATCCGTTTAATCAATATCACCCAAGCC---GCCGCAAAATAGGACAGCTCG     1566

Qy   123 ValLysLysTrp   130
         :::  :::  :::
Db  1567 TTAAAAATTTCAAAAACATCGCGCCTCACGGACAGCTTGGATTACTTGGAAGAGAAAAC     1626

Qy   131 Asp------   145                 GlyIleSerThrLysPheGluAspTyrAlaMetSerProArg   145
         :::                            :::::::::
Db  1627 GATAAGGGGGTAATCCCTGGCTTTGAATATTATTTGAAGAGTTTGAAAGAGAAAACAAAGAA   1686

Qy   146 IleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGln   165
         :::            :::::  :::::
Db  1687 ATCAAAAACCACTATGGAAAAAACAAAACAATTAGAGTCATCATC----GGCAACCGCCT   1740

Qy   166 AsnAlaAsnGlyIleMet------   182              GluGlyLeuGluProLeuAsnAlaIleArgVal   182
             :::                                    :::::::::
Db  1741 TATTCAACGCGGCCGTAAAAGCGAAAACGAACAACAAAACCTCACCACCCAAGCTT       1800

Qy   183 ThrGlnGluAlaValTrpTyrTyrSerArgSerAlaProIleSerAspAsnProAspGluSer   202
         :::                                                   :::
Db  1801 GAAAAACGGGTTTATGAAAACTTACGGCAAAATTCCACGCTCAAAAC               1848

Qy   203 PheLysArgGluSerGluSerAsnLeuValSerrThrSerGlnLeuSerLeuMetArgGln   222
             :::                      :::
Db  1849 --AAGAACTCCACACGAGACACGCTCATCCACAGC--                         1899

Qy   223 AlaLeuLys------   231                        GlnLeuIleAspProAsn   231
         :::::::::                                   :::
Db  1900 CTTTTAAAGATAAAGGGGGTGCTAGGCTTTGTGTGACGGGACTTCATTGACTCTAAA     1959

Qy   232 LeuAlaThrLysMetProLysGlnValProAspAspSPheGlnLeuSerIlePheGluSer   251
         :::             :::::  :::
Db  1960 ACGGCGGACGGGTTTAGAAAATGGCTGGGCACAAGAATTTTCG--CACCTTTATGCGCTG   2016

Qy   252 GluAspLysGlyLysAspLysTyrAsnLysGlyTyrGlnAsnLeuSerGlyGlyLeuVal   271
         :::::  :::::::  :::  :::
Db  2017 AATTTGAGAGGCAATGCCAAGACTTCAGGAGGAGGCGA                         2055

Qy   272 ProThrLysProProThrProGlyAspProProMetProProAsnGlnProGlnThrThr   291
             :::
Db  2056 ------AAAAACAAGGAGATGGAATAATTTGATAGCCGGATCCAGGGTGACGGTA         2103

Qy   292 SerValLeu------   299                         IleArgLysTyrAla   299
         :::                                          :::
Db  2104 GCGATCATCTTTTTTGTCAAAGATAAGGACGCGCCCAATCATCATACGATTTTTTACTATATGAA   2163

Qy   300 IleGlyAspTyrSerLysLeuGluGlyLyaAlaThrLeuGlyIleLeuThrGlyAspAsnVal   319
         :::::  :::::::  :::::  :::
Db  2164 GTGGAGGATTTATTTGAAAAGAGAGAGGAGAGAAACTCAACTGCTCCGCTTAATTTGAAAATTG   2223

Qy   320 AsnSerPheGlnAlaArgValPheSerSerAsnAspIleGlyLysGluArgIle------   338    GluLeu   338
         :::                                               :::               :::
Db  2224 GATTCGGTGCCCTTTTAAGGAAAATCACAAAGGCGATTGGATCCACCAAAAGG           2283

Qy   339 SerAspGlyThrThrTyrThrLeuThrGluAsnSerProAlaGlyTyrSerIleAlaGlu   358
         :::  :::      :::::  :::
Db  2284 AATGACGATTTTGAAAAGCTCATCCCTTTGAAAAGAGACAAAAAAAATCAAAAAATATTCAAT   2343

Qy   359 ProIleThrPheLysThrValGlnAlaGlyLysValTyrThrIleIleIleLeuAspGlyLysGlnIle   378
                                                                :::
Db  2344 GCTTATT---TTTGATCTCAATTCAATTCTAATGGGGTGGGTTGAGCGCTTC           2388

Qy   379 GluAsnProAsnLysGluIleValGluValGlyProTyrSerValGluAlaTyrArgAsnAspPheGlu   398
            :::                                      :::::
Db  2389 --CCTTGG------GTGTATAACTTTTTCGCAA                             2412

Qy   399 GluPheSerValLeuThrThrGlnAsnThrAsnTyrAlaLysProPheTyrTyrAlaLysAspAsnLysAsn   418
            :::::                              :::
Db  2413 AAAACTTTAATGCAATCGGGTCGCAAAAC---                             2439

Qy   419 GlySerSerGlnValValTyrCysPheAsnAlaAlaAspLeuLys   432
             ::                                :::::::::
Db  2440 ------TGCATTGACACTTATAAACGCTGATTTGAAGCGCTTCAATGAGCGTTTC       2487

Qy   433 ------SerProAspSerGluAlaSerProGlyGlyGlyLysThrMetThrProAspPhe   448
               :::::::
Db  2488 AGGGGAAGCCTTCAAACAACGCACACGTCAAAGCATAAAGGTATCAAAAAAGTCAGCCGAT---   2544

Qy   449 ThrThrGlyGluValLysTyrThrHisIleAlaIleArgAspLeuTyrThrVal   468
             :::::      :::
Db  2545 ------CGCTACAAGCACACTTAAACGATAAGAGAAATCACCACTGATAAAACG         2589

Qy   469 LysProArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLys   488
         :::::::::           :::  :::::  :::::
Db  2590 AAAATCGCTTGGGACTCGATGGT------TTGAAAAAC------AAAACTCATT---     2628

Qy   489 GlyTyrArgGluLysGlyGlnAlaIleGluGluTyrSerGlyLeuThrGluThrGluGlnLeu--   507
             :::                              :::::::::
Db  2629 ------AAAAATGAAAATCTGCCCAGAAAAGGGGCATGGAGGACGGCGTAAGGTTAGCC     2676

Qy   508 ------ArgAlaAlaThrGlnLeuAlaIleGluTyrTyr------   521          PheThrAspSer   521
               :::                                                    :::::
Db  2677 TTGTATCGCCCTTTTAACAAAACAATGGCTTTATTGGGATAAAAAATTAATAAACAGACAA   2736

Qy   522 AlaGluLeuAspLys------   534         AspLys------   534        LeuLysAspTyrHisGly   534
         :::::::::                          :::                        :::
Db  2737 TCTCAAATTGCCCAAAAATTTCCCGGATAAAAAGCTCCGCAATGTGGTGATCAAATAACTGGT   2796

Qy   535 PheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleIleLeuValGluTyrAlaGln   554
         :::::::::                            :::
Db  2797 GTGGGTAAATGGTAAGAGATTTTAGGCGTCGTTGTGTAAGCGTTATTGTTAGTTTG       2856

Qy   555 AspSerArgAsnProGlnLeuThrAsnLeuAspPhePheIleProAsnAsnAsnLysTyrTyr   574
         :::                :::::::
Db  2857 ATCTCA---CCCAATCAGGCTTACCCCTTTATATTATTAATGAAAATTAATAACAACAGACA   2913

Qy   575 GlnSerLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIleLeuGluArgMetGlu   594
            :::::                                         :::
Db  2914 AACGCTATCAGCGGCTAT------GCGCTCAACCTCTTCAGGAGGCAT             2955

Qy   595 AspLysLysGluValIlePro------   603                       ValThr   603
         :::                                                    :::
Db  2956 TATAAAGATAATAGCTATTACTGAAGAGAAGATTTTTACTATATATTTTATGCGATTTTCCAC   3015

Qy   604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspThrLysAspPhe   623
             :::                      :::::
Db  3016 CATAAAGGCTATTTGGAAAAAATTACAAAACTCTCCGCCAAAGAACGCGCCGA-----     3069

Qy   624 HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr   643
            :::                     :::::
Db  3070 ------ATCGCTTTGAGCGGAAGACTTAAAGAAGAACTCTATGCTGTTAAATTG         3120

Qy   644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrLeuAsnLeuLysHisGly---   662
         :::::      :::::::  :::::
Db  3121 GCCGGAATTGCACCTATGGAAGTGGGGAAAATCCACACAAGCGCTTAAACATAACCTA     3180

Qy   663 ---GluSerLeuThrLeuGluGlnLeuGlyLeuProGluGlyThrLysTyrLeuValAspGluThr   681
            :::                                               :::::
Db  3181 CTAGGACAGTCGCCGAAATGGGAGGGCCTAT------TATGATGTGATCCAAAATGAAAAAG   3231

Qy   682 AspSerGluGlyTyrLysValLys------   689
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Db  874  ACAAGCCAAAAAGGTGCCATTACATTAGGAACACGTATTGACTCTAATAAGAGTTTTCAT  933

Qy  331  ------------AspIleGlyGluArgIleGlu-----------------------------  337
Db  934  TTTTCTGGAAAAGTAAATTTAGTTACAAATATGAAGGGCAATGGAAATGGTGGAGATGGT  993

Qy  338  -----LeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAla---  352
Db  994  ATCGGTTTGCCTTTCACCAGGTGTATTAGGTGAAACAGGGTTAAAACGGTGCGCAGTA  1053

Qy  353  -----GlyTyrSerIleAlaGluProIleThrPheLysValGluAla-----  366
Db  1054 GGTATTGGTGGCTTAAGTAACCCA------TTTGGCTTCAAATTAGATAACGTTCACAAT  1107

Qy  366  ----------------------------------------------------------  366
Db  1108 ACATCTACGCCAAAATTCATCACCAAAAGGCGAAAGCTGACCCAATCTAAGTGGGTGGA  1167

Qy  367  -------------GlyLysValThrThrIleIleAsp-------------  374
Db  1168 GGTGCCGTTGGTGGCCTTTGTAACACAGAAGTGTTGCCATCAACATATACATCA  1227

Qy  375  GlyLysGlnIleLeuGluAsnProAsnLysGluIleValGlyProTyrSerValGluAlaTyr  394
Db  1228 AGTTCAACAGCTGATAATGCTCCGCAAAAGTTAAAATGTTCAAACACTACAAAC-  1275

Qy  395  AsnAspPheGluGluPheSerVal-----------------------------  407
Db  1276 AACACGTTCCAAGATTTTGATATTAATTATATAAATGGTGATACAAAAGTTATGACCGTTAAA  1335

Qy  408  TyrAlaLysPheTyrTyrTyrAlaLysAsn-------------------------------  421
Db  1336 TATGCAGGTCAAACATGGACACGTAATATATTTCAGATTGGATTGCGAAAAGTGGTACGACC  1395

Qy  422  GlnValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyGly  441
Db  1396 AACTTTTCATTATCATTATCAATGACACGCC-----------TCAACAGGTGGC  1431

Qy  442  LysThrMetThrProAspPheThrThrGlyGluValAlaLysThrTyrThrHisIleAla-  459
Db  1432 GCGACAAATTTACAACAGATACAAATTGGACAATTCGAATATACAGAATTCGCTGTTACA  1491

Qy  460  ----------------------GlyArgAspLeuPheLeuLysTyrThrValLysPro  470
Db  1492 CAAGTGAGATACGTTGATGTAACAACACAGGTAAAGATATTATT-----------------  1533

Qy  471  ArgAspThrAspProAspThrPheLeuLysHisIleLysLysValIle------------  486
Db  1534 ---CCCCAAAAACATATTCTGGAAATGTTGATCAAGTCGTGACAAATCGATAAT  1584

Qy  487  -----------GluLysGlyTyrArg------------GluLysGlyGlnAla  496
Db  1585 CAACAATCTGCATTGACTGCTGCTAAAGGATAACTACACATCTGTCGAAGTCATATGCA  1644

Qy  497  IleGluTyrSerGlyLeuThrGluThr---------GlnLeuArgAlaAlaThrHrgLeuAlaIle  515
Db  1645 TCAACTTATAAGATACAAAATAAAACTGTAAAAATGACGAATGCTGGACAATCAGTGACA  1704

Qy  516  TyrTyrPheThrHrgAspSerAlaGluLeuAspLysLysAspTyrHisGlyPhe  535
Db  1705 TATTATTTTTACT-------------------------------------------  1716

Qy  536  GlyAspMetAsnAspSerThrLeuAlaLysIleLeuValGluTyrAlaGlnAsp  555
Db  1717 --GATGTAAAAGCACCAACTGTAACTGTAGGCAATCAACCATTGAAGTGGGTAAAAACA  1773

Qy  556  SerAsnProProGlnLeuThrAspLeuAsp-------------------  565
Db  1774 ATGAATCCTATTGTGTTTGACTACAACAGATAATGGTACAGGGGACTGTGACAAATACAGTT  1833

Qy  566  PhePheIleProAsnAsnAsnLysTyr------------GlnSerLeuIleGlyThrGln  581
Db  1834 ACAGGAGATTACCAAGCGGGATTAAGTTATGATAGTGCAACGAATTCAATCATTGGGACACCA  1893
```

```
Qy  582  TrpHis---ProGluAspLeuValAspIleIleArgMetGlu-----------AspLysLysGlu  598
Db  1894 ACAAAAATTGGTCAATCAACAGTGACAGTAGTACTACTGACCAAGCAAATAACAAATCG  1953

Qy  599  ValIleProValThrHisAsnLeu-----ThrLeuArgLysThrValThrGlyLeuAla  616
Db  1954 ACGACAACTTTTACAATAAATGTTGGATAACGACAGCACCAACAGTGACGCCAATA---  2010

Qy  617  GlyAspArgThrLysAspPheHis----------------PheGluIleLeuLeuLysAsn  631
Db  2011 GGAGATAAAATCATCAGAAGTTTTTCCCAATATCACCGATTAATATTGGTACGGAGGAC  2070

Qy  632  AsnLysGlnGluLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLys  651
Db  2071 AATAAGTGGTAAATGCAGTAACAAATACAGGTACCAGGATTCCCGTCTGGATTAAACATTC--  2127

Qy  652  AspGlyLysAlaThrIleAsnLeuLeuLysHisGlyGluSerLeuThrLeuGlnGlyLeuPro  671
Db  2128 ------GATAGCACAAATAAT--------------ACTATTAGTGGGTACACCA  2160

Qy  672  GluGlyTyr-------SerTyrLeuValLysGluThrGluGlyTyrLysVal  688
Db  2161 ACAAACATTGGTACAAGTACTATTACAATCGTTTCTACAGATGCCGAGTGGTAACAAACG  2220

Qy  689  LysValAsn---SerGlnGluValAlaAsnAlaThrValSerLysThrHrgGlyTyrIleThrSer  707
Db  2221 ACAACCACTTTTAAATATGAAGTAACAACAGAAATAGCCATGAGTGATTCCGTATCAACACATCG  2280

Qy  708  AspGluThr  710
Db  2281 GGAAGTACC  2289
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RESULT 13
US-09-815-242-7425
; Sequence 7425, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7425
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS

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Db  612 ---------------------ACGAAACGC------------------TTAGCAGGC--- 629
        |||     |||                     ||||||||||
Qy  619 ArgThrLysAspPheHisPheGluIleLeuLeuLysAsnAsnLysGlnGluLeuSer 638

Db  630 ---------------GCAGAATTTACATTGAAAGATGTGAAAAGGCAATGTTGTAAAA 671
        |||||||||||                   ::::     :::
Qy  639 GlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsn 658

Db  672 GAAGGAATTACAACAGATAAAGTCTGGA------------------------ 698
        ||||||||                      ::::
Qy  672 ValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGlu 671

Db  699 -----------ACTGTTAAAGTAGACGGACTTGTGCCGGGGT--GAATATACGTTA 740
                ::::    ||||||||          |||      ::    |||::
Qy  659 LeuLysHisGlyGluSerLeuThrLeuGlnGlyLeuProGlyGlyTyrSerTyrLeuVal 678

Db  741 GAAGAAAACAAAACGCCCAGAAGGTTATAGGCATTAGAAGTAACAATCGAAAGACGTA 800
           ||||     ||||         |||         :::    |||
Qy  695 ValAlaAsnAlaThrValSerLeuLysThrGlyIleThrSerAspGluThrLeuAlaPheGlu 714

Db  801 GTAGCAAACAAGAGTAGTA-- 818
        ||||||||
Qy  701 GluGlyLeuGlnAlaLeuArgLeuLeuLeuAsnGlyLysLeuLeuSerAlaPheProLeuGly 725
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```
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(7035)
US-09-815-242-8615

Alignment Scores:
Pred. No.:                    0.00214
Score:                        144.50
Percent Similarity:           31.63%
Best Local Similarity:        19.05%
Query Match:                  3.66%
DB:                           9

Length:         7035
Matches:        153
Conservative:   101
Mismatches:     298
Indels:         251
Gaps:           38
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US-09-494-297-2 (1-757) x US-09-815-242-8615 (1-7035)

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Qy   79 ValArgGlyHisProThrTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98
           :::          ||| |||         ::: ||| ||       |||
Db  121 ATAATGGGACTACCAGTTTATTAATTAGTCATTAGTATGGTGAGTCAAGAT--------- 165

Qy   99 GluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGly 118
         |||     |||                   :::  |||||      ||| :::
Db  166 AATCAAAGCATTAGTAAAAAAAATGACTGGATACCGGACTGAAAACGACGGCAGTGATCGGC 225

Qy  119 SerAspSerSerValLysThrTrpTyrLysLysHisAspPheGlyIleSerThrLysGlu 138
             ::: |||    |||               |||::: |||
Db  226 GGGCGTTTCACGGTAAAC---ATCTTGCATGACCAG------------------CAA 261

Qy  139 AspTyrAlaMetSerProArgIleThrGlyValAspGluLeuAsnGlnLysLeuArgAlaVal 158
            |||       ::: |||   |||          ||| |||::: |||
Db  262 GCTTTTGCGCGTTCTGATGCACCATTAACATCTGAATTAAATACACAAAGTGAAACAGTA 321

Qy  159 MetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuLeuGluProLeuAsn 178
            |||                   ||| ::       |||
Db  322 -------GGTAAT---CAAAATTCAACACACAATCGATCGATCATCAACATCAACACCGAT 369

Qy  179 AlaIleArgValThrGlnLeuAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn 198
           |||                ::: |||          ::
Db  370 TCCACAAGCGTAACGTAACGAAAAAT--------------------------- 414

Qy  199 ProAspGluSerPheLysSerArgGluSerGluAsnLeuValSerThrSerGlnLeuSer 218
           |||   |||  :::     |||  ||||||               :::
Db  415 AGTGACACAGTCTCAAGTGAGAAAGTCTGAA----AATGTCACTTCGACAACTAATAGTACA 471

Qy  219 LeuMetArgGlnAlaLeuGlyIleLeuIleAspProAsnLeuAlaThrLysMetProLys 238
            ||| |||        ||||||    :::     :::       |||||
Db  472 AGCAATCAACAA------GAAAAATTGACATCTACATCACAGAATCAACATCCTCAAAGAAT 525

Qy  239 GlnValProAspPheProGluGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyr 258
               :::   |||          |||  :::::||
Db  526 ACTACATCAAGTTCTGATACTATAAATTCTCAACTTCAACAGTACACGAACAACAACAATT 585

Qy  259 AsnLysGly---TyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThr 277
           ||| ||| |||             :::   ||| ||||
Db  586 AATACATCAACAAATTCAAAGTACTGCATCAAATAACACACTTCACAAAGCACAACGGCCAACT 645

Qy  278 ProGlyAspProProMetProProAsnGlnProGlnThrThrSerValLeuIleArgLys 297
           |||   |||               |||              |||
Db  646 TCAGCCAAC------TTAAACAAAACTAGCACACTACAGCGTCAACTACTACACTCCGCCA 693

Qy  298 TyrArgIleGlyAspTyrSerLysTyr---------------- 306
            |||                 |||
Db  694 GTAAAACTTCGAACTTTCAGTCGCTTAGCTATGTCAGCAGCGACGACA 753

Qy  307 -----LeuGluGlyValAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGln--- 323
             |||                  ||| :::
Db  754 ACCGCATTAACTGCTAATACAATTACAGTTAATAAAGATAAACTTAAAAACAATATATGACA 813

Qy  323 -------------------- 323
Db  814 ACTTCAGGTAATGCCACTTATGACCAAAAGTACAGGGGTCGTAACGTTAACGGACAGATACA 873

Qy  324 ------------------------AlaArgValPheSerSerAsn-------- 330
                                      |||::: :::
```

```
Db  2638  ACATCAAACACAGGTCGTCATTAAAGAGTAAAGATAAACGATACTATTGACTCTGGTTTCTAC  2697
Qy   529  ---------------LeuLysAspTyr--------                    HisGlyPheGly  536
Db  2698  AAACCGACTTACACTTAGGTGACTATGTATGGGAAGATACAAATAAAAACGGTGTTCAA  2757
Qy   537  AspMetAsnaspSerThrLeuAlaValAla----                                  Lys  547
Db  2758  GATAAAAGATGAAAAGGCATTTCAGGTGCTAACAGTTACGTTAAAAGATGAAAAACGACAAA  2817
Qy   548  IleLeuValGluTyrAlaGlnAspSerAsnPro---          GlnLeuThrAspLeuAspPhe  566
Db  2818  GTTTTAAAAACAGTTACAACAGATGAAAAATGGTAAAATATCAATTCACTGATTTA---  2871
Qy   567  PheIleProAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAsp  586
Db  2872  --------AACAATGGAACTTATAAA--  2889
Qy   587  LeuValAspIleIleLeuArgMetGluAspLysGlyGluValIlePro-----      ValThrHis  604
Db  2890  -------GTTGAATTCCGAGACCATCAGGTTATACACCACTTCAGTAACTTCT  2937
Qy   605  AsnLeuThrLeuArgLys-------------      ThrValThrGlyLeu------   ---Ala  616
Db  2938  GGAAATGATACTGAAAAAGATTCTAATGGTTTAACAACACAGGGTGTCATTAAAGATGCA  2997
Qy   617  GlyAspProArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeu  636
Db  2998  GATAACAATGACATTAGACAGTGGTTTC------  3048
Qy   637  ------LeuSerGlnThrValLysThrAspLysThrAsnLeuGlu  649
Db  3049  GGTGATTATGTTGGTACGACAGTAATAAAGACGGCAAACAAGATTCAACTGAAAAAGGT  3108
Qy   650  PheLysAspGlyLysAlaThrIleAsnLeuHisGlyGluSerLeuThrLeuGlnGly  669
Db  3109  ATCAAAGATGTTAAAGTTACTTTATTAAATGAAAAAGGCGAAGTAATTGGAACAACTAAA  3168
Qy   670  LeuProGluGlyTyrSerTyrLeuValLysGluThrGlyGlyThrTyrLysLysValLys  689
Db  3169  ACAGATGAAAAATGGTAAAATACTGCTTTGATAATTTAGATACGGTAAAAACAAAGTTATT  3228
Qy   690  ValAsnSerGlnLeuValAlaIleAsnAlaThrHrValSerIleLysThrGlyIleThrSerAspGlu  709
Db  3229  TTT------GAAAAGCCTGCTGGCGTTAACACAGTTACAAAATACAAACACAAAGATGAT  3282
Qy   710  ThrLeuAlaPheGluAsnAsnLysGlyLeuSerGluProValValaProThrGlyValAspGlnLysIle  729
Db  3283  AAAGATGCAGATGGTGCGGAAGTGACGTAACAATTACGGATCACATGATGATTTCACACTT  3342
Qy   730  ---AsnGlyTyr  732
Db  3343  GATAACGGATAC  3354
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US-09-842-552-98

Alignment Scores:
Pred. No.:
Score: 146.50
Percent Similarity: 35.14%
Best Local Similarity: 21.69%
Query Match: 3.71%
DB:

Length: 2522
Matches: 100
Conservative: 62
Mismatches: 112
Indels: 187
Gaps: 23

US-09-494-297-2 (1-757) x US-09-842-552-98 (1-2522)

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Qy   305  LysLeuLeuGluGlyAlaThrArgLeuGlnLeuGlyAspAsnValAsnSerPheGlnAla  324
Db    57  CAACTTCTACCAGGTGCAAAATTTGATGTTATCCGATAAAGATGGGAAAGTTGTGGAAACA  116
Qy   325  ArgValPheSerSerAsnAspIleGlyGluArgIle------GluLeuSerAspGlyThr  342
Db   117  ATTGTT-----ACAGATGATAAAAGGTGAAGCTTTATCGAAACAACTTCCAGTTGGAAGC  170
Qy   343  TyrThrLeuThrPheGlyLeuAsnSerProAlaGlyTyrSerIle---AlaGluProIleThr  361
Db   171  TATACATTAAAAGAAGTAGAAGCACCGAAAAGGATATGAATTATCATCCAGTTCAGTTTCT  230
Qy   362  PheLysValGlyAlaAlaGlyValLysValThrTyrThrIleIleGluAspGlyLysGlnIleGluAsnPro  381
Db   231  GTTGAATGTAGAGGCTAATAAAGTAAGTGACT---      GTAGATGGTG  272
Qy   382  AsnLysGlyIleGluValGluProTyrSerValGluValAlaTyrAsnAspPheGluPheSer  401
Db   382  TATAAAACACCAAAAATATAGTTTA      GGTTCAATTCGAA  311
Qy   402  ValLeuThrThrGlnAsnThrAsnTyrAlaLysPheTyrArgAlaLysAsnGlySerSer  421
Db   312  GTGGTGAAAGTAGATGCAAATGAAAA      ACGAAATTTGTTATCCGTTGGCAGAA  362
Qy   422  GlnValValTyrCysPheAsn------      AlaAspLeuLysSerProProAspSerGlu  438
Db   363  TTCGGAAGTGTATAAGATGGCAAAAGGTAGCAGAACTGAAA------      ACAGGT  410
Qy   439  AspGlyGlyLysThrMetThrProAspPheThrThrGlyGluValValLysTyrThrHisIle  458
Db   411  GAGAGTGGAAAAGTGATGTCACCGAAAATTACCCCTAGGTGAA------      452
Qy   459  AlaGlyArgAspLeuPheHisLysTyrThrValLysProArgAspThrProPhe  478
Db   453  ------      TACACAGGTGAAA------  464
Qy   479  LeuLysHisIleLeuLysLysValIleGluGluLysGlyTyrArgGluLysGlnAlaIleGlu  498
Db   465  ------      GAAACGAAAGCACCAGCGCGGCTACAAGCTTTCAGATAAGAAGAATGG  509
Qy   499  TyrSerGlyLeuThrGluThrGlnIleLeuArgAlaAlaAlaThrGlnLeuAlaIleTyrTyrPhe  518
Db   510  AAAGTAACAATTCAAAACGAGAAAGAA-----      536
Qy   519  ThrAspSerAlaGlyLeuAspLysLysAspTyrHisGlyPheGlyAspMet  538
Db   537  -----      GTTGTAAAAGTAGAGGCAGAA-----  557
Qy   539  AsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnPro  558
Db   558  -----      GTAGTAAAAGTAGAGGCAGA-----  578
Qy   559  ProGlnLeuThrAspLeuAspPheIleProAsnAsnLysTyrGlnSerLeuIle  578
Db   579  -----      AACGAAAAA-----  598
Qy   579  GlyThrGlnTrpHisProGluAspLeuValAspIleIleLeuArgMetGluAspLysGlyGlu  598
Db   599  -----      ATCTTA-----  618
Qy   599  ValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspTyrGluAspLys  618
Db   611  GGTTCT      CTACAAAATTAATTAAAATATGGATGGATAAAAGATCAA  611
```

```
Qy    26  PheThrValThrLeuValGlyValPheAlaLeuValThrSerMetVal              45
                   :::   |||   ::::
Db   682  TTGAATACAAGA------ATGGTATAGCAGCAGTACAGCCATCATCAACA           726

Db    46  GlyAlaLysThrValPheGlyLeuValSerSerThrPro-----                 59
                   |||               :::::|||
Qy   727  GAGGCTAAAAAGTTGTAAATGATTTAATCACATCAAATAACAACATGTCGTTGATGCA   786

Qy    60  ------AsnAlaIleAsnPro------AspSerSerGluTyrArgTrpTyrGly        74
Db   787  GATAAAAAACAATAAAATCGTACCAGCCCAAGATTATTTATCATTAAAATCACAAATTACA 846

Db    75  TyrGluSerTyrTyrValArgGlyHisProTyrTyrLysGlnPheArgValAlaHisAspLeu 94
                   |||                :::::
Qy   847  GTTGATGACAAAGTTAAATCAGGTGATTATTTC-----                       879

Db    95  ArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLysAla 114
                   :::::|||||||||
Qy   880  ------ACAATTAAATACTTCAGATACAGTACAAGTATATGGATTGAATCGGAAGATATT  933

Qy   115  PheProLeuGlySer------AspSerSerValLysLysTrpTyrLysLysHis       130
Db   934  AAAAAATATTGGTGATAATTAAAGATCCAAAATAATGGTGAAAACAAATTGCGACTGCAAAACAT 993

Db   131  AspGly------IleSerThrLysPheGluAspTyrAlaMetSerProArgIle       146
                   |||||||||      :::::|||
Qy   994  GATACTGCAAATAATTAATTACACATTACAGATATAGTT-----                 1038

Qy   147  ThrGlyAspGluLeuAsnGlnLysLeuArgGlyAlaValMetTyrTyrAsnGlyHis---- 163
Db  1039  GGATCGGATTTAATTCTGTACAAATGGGAATTAATTATTCAATTTATATGGATGCT     1092

Db   164  ProGlnAsnAlaAsnGlyIleIleMetGluGlyLeuGluProLeuAsnAlaIle        180
                   :::   |||
Qy  1093  GATACAAGTTCCTGTTAGTAAAAACGGATGTGAGTTTAACAAATGCCAAACTAAAACTACA 1152

Db   181  ArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAlaProAsnProAsp 200
                   |||   |||||||
Qy  1153  ACAAAACAAACTGCTACAACATTCAATATATCCAGATTAGTGTGTAAATGAGAAAAATTCAATT 1212

Qy   201  GluSerPheLysArgGluSerGluSerAsnLeu------                       211
Db  1213  GGATCAGGGTTCACTGAAAACAGTTTCACATGTTGGAAATAAAGAAAAATCCAGGTACTAT 1272

Db   212  ------ValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLys---           225
                   |||   |||||||
Qy  1273  AAACAAAAACGATTTATGTAAAAAATCCATCGGAAAAAATTCTTTAACAAAATGCCAAACTAAAAGTT 1332

Qy   226  ------GlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnIleValProAsp  242
Db  1333  CAAGCTTACCACTCCAAGTTATCCTAATAATATCGGGCAAATAAATGTAACAGAT       1392

Db   243  AspPheGlnLeuSerIlePheGluSerGluAspLysSerGlyTyrAsnLysGlyTyr     262
                   |||||||
Qy  1393  ------ATAAAAAATATATCAA------GTTCCTAAAGGTTTATACATTAAATAAGGATAC 1440

Qy   263  GlnAsnLeuLeuSerGlyGlyLeuValProThrGlyProProThrGlyAspProPro     282
                   |||||||
Db  1441  GAT------GTGAATACTAAAGAGCTTACA-----                           1464

Db   283  MetProProAsnGlnProGlnThrThrSerValLeuLeuIleArgLysTyrArgAlaIleGlyAsp 302
                   :::::|||||          |||||||
Qy  1465  ------GATGTAACAAATCAATACTTCGAAAATACATATGGCGAC                 1506

Qy   303  TyrSerLys-----                                                305
Db  1507  AACAATAGCGCTGTGTTATTTGGAAATGCAGATTTGCTTATGTTGTTAATGGTTAAT    1566

Db   306  ------LeuLeuGlyIleAlaThrLeuGln                                313
                   |||||||||||||
Qy  1507  AACAATAGCGCTGTGTTATTTGGAAATGCAGATTTGCTTATGTTGTTAATGGTTAAT    1566

Qy   314  LeuThrGlyAsp-----                                             317
Db  1567  ACAAAAATTCCAAATATACAAAATACGGAAAAGCCCAACACTTGTTTCAAAATGGCTACTTTATCT 1626

Db  1627  TCAACAGGTTAAATAAATCCGTTTCTACTGGCCAAATGCTTTTAGGATTTACTAACCAAAGT 1686

Qy   318  SerAsn------AspIleGlyLeuArgIleLeuSerAspGlyThrGlyThrLeu        345
                   ::::|||
Db  1687  GGCGGAGCTCGGTCAAGAAGTATATAAAAATTGGTAACTACGTATGGGAAGGAGATACTAATAAA 1746

Qy   320  AsnSerPheGln------AlaArgValPheSer                             328
                   |||
Db  1747  AACGGTGTTCAAGAATTAGGAGAGAAAAAAGGCGTTGGCAAATGTAACTGTAACTGTATTTGAT 1806

Qy   346  ThrGluLeu------AsnSerProAlaGlyTyrSer                          355
                   |||||||               |||||||
Db  1807  CCAAACTTACCTAATGGAAATTTTCAAACTTACCAAAAAGGTTATGAA             1866

Db   356  IleAlaGlu------                                               358
Qy  1867  CCAAATTACAACAAGTAGGAGATTTCCGTTGTAAGAAAGCAGTTACTACTTTGAATT    1926

Db  1927  GTAACCCCTTCAAAAAACAAAGGTAATAACGAAGAATTAGATTCAAACGGCTTACTTCAGTT 1986

Qy   359  ------ProIleThrPheLysValGlnAlaGlyLysValTyr-----              370
                   :::::|||       |||
Db  1987  ATTACAGTTAATGGCAAAAGATAACTTATCTGCAGACTTAGGTATTTTACAAACCTAAAATAC 2046

Qy   371  ------ThrIleIleAspGlyLys------                                377
                   :::|||                Gln
Db  2047  AACTTATGTGACTATGTCTGGGAAGATACAAATAAAAATGGTATCCAAGACCAAGATGAA 2106

Qy   378  IleGluAsnProAsnGlyGluValGlnProTyrSerValGluLeuAlaThrTyrAsnAspPhe 397
                   |||   :::||           |||||:::|||
Db  2167  GTTACAACAGACGCTGATGCAAATAATAATTACTGATTTCATCATATAGTAATTATAAA 2226

Db   398  GluGluPheSer------ValLeuThrThrGlnAsnTyr-----                  408
Qy  2227  GTTGAATTTACTACACCAGAAGGCTATACACCAGACATCGTGATACCGGTGACGGTGACAATT 2286

Qy   409  ------AlaLysPheTyrTyrAlaLysAsnGlySerGlnValValTyrCys          426
                   |||:::||||        |||
Db  2287  GAAAAAGACTCTAAATGGTTTTAAACACAGTTTTAATGGTGCTGAATTAACAGACA     2346

Db   427  PheAsnAlaAspLeuLysSerProProAspSerGluAsp------GlyGlyLysThr     443
                   :::||||               |||
Qy  2347  TTAGATAGTGGATTCTACAAAACCACCAAAATTAATGGTAATTTATGTGGGAAGGAGAT   2406

Qy   444  MetThrProAspPheThrThrGlyLeuValLysTyrThrHisIleAlaGlyAlaArgAsp-- 462
                   ::::|||
Db  2407  ACAAATAAAGATGGTAAGCAG------GATTCAACTGAAAAAGGTATTACCAAATGGTAACA 2460

Db   463  LeuPheLysTyrThrValLysProArgAspProAspThrPheLeuLysHisIle        482
                   |||||||
Qy  2461  GTTACATTGAAAAAATGAAAAACGGTGAAGTTTTTACAAACAACTAAAACAGAATAAAGATGGT 2520

Qy   483  LysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyr-----       499
                   |||||||
Db  2521  AAAATCAAATTTACT------GGTAGTAAAATGGACACTTATATAAAAGGTAACACCA       2535

Db   500  SerGlyLeuThrGluThrGlnLeuArgGlnAlaLaThrGlnLeuAlaIle------TyrTyrPhe 518
                   |||||||:::           |||
Qy  2536  ------GGTTAGAAAATGGAACTTGATATTATGAACGGTGAAGTTTATAGATTTCAAAATGGT 2577

Qy   519  ThrAspSerAlaGluLeuAspLysAspLys------                          528
                   |||       :::       |||||||||
Db  2578  TCAGGTTACACACCAACCACAAGCAAGTAGGTTCAGGAACTGATGAGGGTATAGATTTCAAAATGGT 2637
```

```
Qy   378 IleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaThrTyrAsnAspPhe 397
            ::|||        |||        :::|||        :::|||
Db  2227 GTTGAATTACTACACACCAGAAGGCTACACCGACTACAGTAACACTCTGGTAGCGACATT 2286

Qy   398 GluGluPheSer---ValLeuThrThrGlnAsnTyr------------ 408
            |||::||    |||||||||||
Db  2287 GAAAAAGAGACTCTAATGGTGTTAACACAACAGGTGTTATTAATGGTGTTGATAACATGACA 2346

Qy   409 -----AlaLysPheTyrTyrAlaLysAsnLysGlySerSerGlnValValTyrCys 426
            :|||        |||        |||
Db  2347 TTAGATAGTGGATTCTACAAAACACCAAAATATAATTTAGGTAATTATGTATGGGAAGAT 2406

Qy   427 PheAsnAlaAlaSpLeuLysSerProProAspSerGluAsp------GlyGlyLysThr 443
            |||        :::        |||
Db  2407 ACAAATAAAGATGGTAAGCAG-----GATTCAACTGAAAAAGGTATTCAGGCGTAACA 2460

Qy   444 MetThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAsp-- 462
            ||||||||||     |||        ::|||||
Db  2461 GTTACATTGAAAAAATGAAAAACGGTGAAGTTTTACAAACAGATAAAGATGGT 2520

Qy   463 LeuPheLysTyrThrValLysProArgAspThrAspThrPheLeuLysHisIle 482
            |||        |||        |||
Db  2521 AAATATCAATTTACT------------ 2535

Qy   483 LysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyr------- 499
            :::|||||        |||
Db  2536 ----------GGATTAGAAAATGGAACTTATAAAGTTGAATTCGAAACACCA 2577

Qy   500 SerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuLeuAla---TyrTyrPhe 518
            |||||||||        ::|||        |||
Db  2578 TCAGGTTACACCACAACACAAGTAGGTTCAGGAACTGATGAAGGTTATAGATTCAAAATGGT 2637

Qy   519 ThrAspSerAlaGluLeuAspLysAspLys----------------- 528
            |||||||||
Db  2638 ACATCAACAACAGGTGTCATTAAAGATAATAACGATACTATTGACTCTGGTTTCTAC 2697

Qy   529 -------LeuLysAspTyr------------HisGlyPheGly 536
            :::|||||
Db  2698 AAAACCGACTTACAACTTAGGTGACTACGTATGGGAAGATACAAAATAAAAACGGTGTTCAA 2757

Qy   537 AspMetAsnAspSerThrLeuAlaValAla--------Lys 547
            |||||||        ::|||
Db  2758 GATAAAGATGAAAAGGCATTCAGGTGTTAACAGTACGTTAAAGATGAAAAACGAACAA 2817

Qy   548 IleLeuValGluTyrAlaGlnAspSerAsnProPro---GluLeuThrAspLeuAspPhe 566
            :::||||        |||||||||||
Db  2818 GTTTTTAAAAAACAGTTACAACAGATGAAAAATGGTAAAATCAATTCACTGATTTA--- 2871

Qy   567 PheIleProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGlyAsp 586
            ||||||
Db  2872 --AACAATGGAACTTATAAA------------------- 2889

Qy   587 LeuValAspIleIleArgMetGluAspLysLysGluValIleIlePro-----ValThrHis 604
            :::        |||
Db  2890 --------GTTGAATTCGAGACACCATCAGGTTATACACCAACTTCAGTAACTTCT 2937

Qy   605 AsnLeuThrLeuArgLys-------------ThrValThrGlyLeu-------Ala 616
            |||        ||||||||:::
Db  2938 GGAAATGATACTACTGAAAAGATCTTAACGACAACACAGGTGTTCATTAAAGATCCA 2997

Qy   617 GlyAspArgThrLysAspPheHisPheCysLeuLeuLysAsnAsnLysGlnGluGlu 636
            |||        :::        |||
Db  2998 GATAACAATGACAATTAGACAGTGGTTTC------------TATAAAAACACCAAAAATATAGTTTA 3048

Qy   637 ----------------LeuSerGlnThrValLysThrThrAspLysThrAsnLeuGlu 649
            |||        ::::::
Db  3049 GGTGAATTATGTTGGTACGACAGTAATAAAAGACGGCAAACAAGATTCAAACTGAAAAAGGT 3108

Qy   650 PheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeuGlnGly 669
            |||        |||        |||        |||
Db  3109 ATCAAGAATGTTAAAGTTACTTTATTAAAATGAAAAATAATGCAGATATCATTTTGCCAAAAAAGTACAGCACACCTAAACGT 3168
```

RESULT 10

Alignment Scores:

Pred. No.:		
Score:	147.00	Matches: 203
Percent Similarity:	29.28%	Conservative: 91
Best Local Similarity:	20.22%	Mismatches: 338
Query Match:	3.738	Indels: 372
DB:	9	Gaps: 44
	0.000541	Length: 4050

US-09-494-297-2 (1-757) x US-09-815-242-9039 (1-4050)

```
Qy   670 LeuProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrLysTyrLysValLys 689
            |||        |||        |||        :::
Db  3169 ACAGATGAAAAATGGTAAATACTGCTTTGAATTAGATATTGATAAGCCGGTTAAATACCAAAAGTTATT 3228

Qy   690 ValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu 709
            ||:::        |||        |||||||
Db  3229 GAAAAGCCTGCTGGCTTAACACAACAAACAGTTACAAATAACACAACTGAAGATGAT 3282

Qy   710 ThrLeuAlaPheGluAsnAsnLysGlyProValValProThrHrGlyValAspGlnLysIle 729
            |||        :::        |||
Db  3283 AAAGATGCAGATGGGTGGCCGGAAGTGACGTAACAAATTACGGATCAGATCATGAGATTTCACAACTT 3342

Qy   730 ---AsnGlyTyr 732
            |||||||
Db  3343 GATAACGGATAC 3354
```

```
Qy     8 AsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSer-----LysArg 25
            |||        |||        :::|||
Db   622 AATTCAAATAAATAATGAAAATAATGCAGATATCATTTTGCCAAAAAAGTACAGCACACCTAAACGT 681
```

```
; PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 4843
SOFTWARE: FastSEQ for Windows Version 4.0

US-09-815-242-4843
; ORGANISM: Staphylococcus aureus
; TYPE: DNA
LENGTH: 4047
SEQ ID NO 4843
DB:                                9
Query Match:                       3.73%
Best Local Similarity:             20.22%
Mismatches:                        20.22%
Percent Similarity:                29.28%
Score:                             147.00
Pred. No.:                         0.00054
Alignment Scores:

US-09-494-297-2 (1-757) x US-09-815-242-4843 (1-4047)
```

```
Qy        8 AsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSer----------LysArg 25
            |||||||  || |||||                               |||||
Db      622 AATTCAAAATAATAATGAAAAATAATGCAGATATCAATTTGCCAAAAAAGTACAGACCTAAACGT 681

Qy       26 PheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSerMetVal 45
              :::                                            |||
Db      682 TTGAATACAAGA---------------ATGCGTAPAGACAGCAGTACAGCCCATCACAACA 726

Qy       46 GlyAlaLysThrValPheGlyLeuValGluSerSerThrPro------------- 59
            |||||||  ||  ||                        |||::::::|||
Db      727 GAGGCTAAAAATGTTAATGAATTTAATCACATCAAATACAACTGTCGTTGATGCA 786

Qy       60 ---------AsnAlaIleAsnPro--------AspSerSerGlyTyrArgTrpTyrGly 74
                     ||| |||                       |||
Db      787 GATAAAAACAAATAAAAATCGTACCAGCCCAGATTATTTATCATTAAAATCACAAATTACA 846

Qy       75 TyrGluSerTyrValArgGlyHisProTyrTyrLysGlnProAlaGlyAlaHisAspLeu 94
                                  |||:|||              ::
Db      847 GTTCATGACAAAGTTAAAACGAGGTGATATTTTC------------------------- 879

Qy       95 ArgValAsnLeuGluGlySerArgTyrCysPheAsnLeuLeuLysLysAla 114
            :::::||                 ||||||||        ::
Db      880 -----ACAATTAAATACTCAGATACAGTACAAGTAGTATGGAATGAAGTATAT 933

Qy      115 PheProLeuGlySer----------AspSerSerValLysLysTrpIleLysLysHis 130
                         |||:::::         ||||||
Db      934 AAAAAATATTGGTGATATTAAAGATCCAAAATAAGTTGAAACAAGTTGCACTGCAAAACAT 993

Qy      131 AspGly----------IleSerThrLysPheGluAspTyrAlaMetSerProArgIle 146
            ||||||          |||:|||        |||||||
Db      994 GATACTGCAAATAATTTAATTACAATAACAATTTACAGATTATGTT- 1038

Qy      147 ThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHis--------- 163
              |||                                    :::|||::::
Db     1039 ----GATCGATTTAATTCTGTACAAATGGGAATTAATTATTCAATTTATATGGATGCT 1092

Qy      164 ------ProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIle 180
                  |||              |||
Db     1093 GATACAAATTCCTGTTAGTAAAACGAGTTGAGTTTACGATAGGTAATACTACA 1152

Qy      181 ArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAsp 200
            |||                          :::                       |||
Db     1153 ACAAAAAACAACTGCTAACATTCAATATCCCAGATTATGTTGTAAATGAGAAAAATTCAATT 1212
```

```
Db     1213 GGATCAGCGGTTCACTGAAACAGTTTCACATGTTGGAAATAAATCCAGGGTACTAT 1272
              |||||                 |||:::|||
Qy      201 GluSerPheLysArgGluSerGluSerAsnLeu------------------ 211

Db     1273 AAACAAACGATTTATGTAAAATCCATCGGAAAAATTCTTTAACAAAGTGCCAAAAAAGTT 1332
              |||||:::|||        |||:::|||
Qy      212 ----ValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLys-- 225

Db     1333 CAAGCTTACCCACTCACAGTTTATCCTAATAAATATGGGCAAAATAAATAAAGACGTAACAGAT 1392
            ||||||                |||::::
Qy      226 ------GlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAsp 242

Db     1393 ------ATAAAAATATATCAA--GTTCCTAAAGGTTATACATTAAATAAAAGAGGTATATCT 1440
            :::    ||| |||           |||:::||||
Qy      243 AspPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyr 262

Db     1441 GAT------------------------------GTGAATACTAAAGAGCTTACA------- 1464
            |||                              :::||
Qy      263 GlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPro 282

Db     1465 ------GATGTAACAAAATCAATACTTGCAGAAAAAAAAATTACAATGGTGGCGAC 1506
                  |||:::|||
Qy      303 TyrSerLys------------------------------------AsnVal 305

Db     1507 AACAATAGGCGCTGTTATTGATTTTGGAAATGCAGATTCTGCTTATGTTGTTGAAGGTTAAT 1566
            |||                                  :::
Qy      306 -----------------------------LeuLeuGluGlyAlaThrThrLeuGln 313

Db     1567 ACAAAATTCCAATATACAAATAGGCGAAAAGCCCAACACTTGTTCAAATGGCTACTTTATCT 1626
            ||:::::||       |||:::::                   ||||||||||
Qy      314 LeuThrGlyAsp------------------------------AlaArgValPheSer 328

Db     1627 TCAACAGGTAATAAAAATCCGTTTCTACTGGCAATGCTTTAGGATTTACTAATAACCAAAGT 1686
            ||||||:::|||                          |||
Qy      329 SerAsn-----------AspIleGlyArgIleGluGlnLeuSerAspGlyThrTyrThrLeu 345

Db     1687 GGCGGAGCTGGTCAAGAGAGTATAGTATTTAAAAATTGGTAACTACGTATGGGAGACTACTAAA 1746
            ||||||                                  |||
Qy      346 ThrGluLeu--------------------------AsnSerProAlaGlyTyrSer 355

Db     1747 AACGGTGTTCAGAATTAGGAGAAAAAGGCGTTGGCAATGTAACTGTAATTGAT 1806
            |||:::|||                      :::||
Qy      320 AsnSerPheGln------------------AlaArgValPheSer 328

Db     1807 AATAATACAAATTACAAAATAGTAGGAGAAAGCAGTTACTAAAAGAAGATGGGTCATACTTGATT 1866
              :::                                          ::
Qy      356 IleAlaGlu-------------------------------------- 358

Db     1867 CCAAACTTACCTAATGGAAGATTACCGTGTAGAATTTTCAAACTTACCAAAAGGTTATGAA 1926
            ||:::||                      ||| |||
Qy      358 ---------------------------------------------- 358

Db     1927 GTAACCCCTTCAAAAACAAAGGTAATAACGAAGAATTAGATTCAAACGGCTTATCTTCAGTT 1986
            |||||||                              |||||||
Qy      356 IleAlaGlu-------------------------------------- 358

Db     1987 ATTACAGTTAATGGCAAAGATAAACTTATCTGCAGACTTAGGTATTTACAAACCTAAATAC 2046
            |||                                          |||
Qy      358 ThrGluLeu------------------------------------- 358

Db     2047 AACTTATGTGACTATGTCTGGAAGATACAAATAAAAATGGTATCCAAGACCAAGATGAA 2106
            |||||                                       |||
Qy      359 --------ProIleThrPheLysValGluAlaGlyLysValTyr----- 370

Db     2107 AAAGGTATATCTTGGCCGTAACCGTAACATTAAAAAGATGAAAAAACGGGTGACGTGTTAAAAACA 2166
            |||                           :::      |||
Qy      371 -----ProIleIleAspGlyLys-------------------------Gln 377

Db     2167 GTTACAACAGACGCGCCTGATGCAAAATATAAAATTTACTGATTTACATAATAATGGTTAATTATAAA 2226
            |||||||||||                   :::
Qy      181 ThrIleIleAspGlyLys----------------------------Gln 377
```

```
Qy   1279  ATTGCTAATATTATAAAGGGTTGCCTAGTGTGGAGACTATATTTTAAAGAAATAGAGGCGCCA  1338
                      |||    |||:::
Db    253  ---------AspLysGlyAspLysTyr----------  259
                      |||||
Qy   1339  CGACCGTATACATTTGATTAAGGATAAAGGATAATCCGTTTACTATGAAAGATACAGAT  1398
           ::||||||||                          |||
Db    260  LysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu------------ValPro  272
                                                 :::        |||
Qy   1399  CAGGGATATTTTACGACTATTGTAAAAATGCAAAAAGCAATAGAAAAAAAGATGTTTTCT  1458
           ::||||||||
Db    273  ThrLysProProThrProGlyAspProMetProProAsnGlnProGlnThrThrSer  292
                      |||                              |||   |||
Qy   1459  GCTCAAAAAGGTTTGGGAGGCACTCAAAAAGTCAAACCA----------  1500
           :::                                    ------ACG  1500
Db    293  ValLeuIleLeuArgGlyGlyTyrAlaIleGlyLyAspTyrSer----------  304
                       |||                              |||
Qy   1501  ATTTTATTTCAAGGTGTACAAACAGATCAAAAATACAACACCAGTAGACAAAGCA  1560
                                               |||
Db    305  ---LysLeuLeuGlnGlyIyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPhe  322
                |||   |||||                             |||:::|||
Qy   1561  GAGAGTTAAAAAAATTAGAGATGGAAACGACAAAAGTGACATGGTGTCTAATCTT------  1611
                  |||||||                             |||:::
Db    323  GlnAlaArgValPheSerSerAsnAsp---IleGlyGluArgIleGluLeuSerAspGly  341
                       |||||||                       |||:::|||
Qy   1612  AAAAAAAGAAAAATGGTTAGTGGTTACTAATACTGAAAAACCAATCACAACACATCAATT  1644
                                                    Pro Ile----ThrPheLysVal  364
Db   1702  Pro Ile----ThrPheLysVal  364
```

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 44
; LENGTH: 3827
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3702)
; OTHER INFORMATION:
; US-09-870-759-44

Alignment Scores:

Pred. No.:
Score: 148.00
Percent Similarity: 34.48%   Matches: 166
Best Local Similarity: 19.67%   Conservative: 125
Query Match: 3.75%   Mismatches: 292
DB: 10   Indels: 263
                                       Length: 3827
                                       Gaps: 43

RESULT 8
US-09-870-759-44
; Sequence 44, Application US/09870759
; Patent No. US20020175551A1

US-09-494-297-2 (1-757) x US-09-870-759-44 (1-3827)

Qy   64 ProAspSerSerGluThrTyrArgTrpTyr----------GlyTyrGluSerTyrVal 79
          ||::: |||||||:::| ||||||||||
Db   694 CCAGAGAGTACGGACACAATGTACGATGGTTTTTTAAAATAATTAACAATGAAAAGTTATTGTA 753

Qy   80 ArgGlyHisProTyrTyrLys----------------------GlnPheArgValAlaHis 92
          |:::||||||||| ||:||||||
Db   754 TCGAA-AGATAATTACTAAAGGATCACAGATTCAAGGTGGACAGCAGTTAGATTAAGCAC 812

Qy   93 AspSerLeuArgValAsnLeuGluGlyLysSerArgSerTyr------------GlnValTyrCys 108
          |||:::|||||||:::|| |||::: |||||||
Db   813 A--TTAAACATTAAGTGACAGGTACACATACCAATTATTATATAGTGGACAAAGTGCAATT 870

Qy   109 PheAsnLeuLysLysAlaPheProLeuGlySer-------------------------- 119
          |||:::||||||:::
Db   871 ACTGATTTTGAAAAGCCTTCCA--GGTTCTAAAATAACTGTTGATAATACGAGAGAAC 927

Qy   120 -----AspSerServalLysLysTrpTyrLysLysHisAspGlyIleSerThrLysPhe 137
             :::|||||:::||||||||| |:::|||||||
Db   928 ACAATTGTAACAATTCCACAAGGCTACGGTCATAATAATAGTTTTTCAATTAACTAC 987

Qy   138 GluAspTyrAlaMetSerProArgIleThrGly--------------------------- 148
           :::|||||||
Db   988 AAA-------------------------ACCAAAATTACGAATGAACAGCAAAAAGAAGAGTTTGTTAATAAT 1032

Qy   149 --AspGluLeuAsnGlnLysLeuArgAlaVal 158
                                                     :::||||:::
Db   1033 TCACAAGCTTGGTATCAAGAGCATGTGTAAGGACATGGAAGAAGTTGAAGACGGGAAA----------TCATTT 1086

Qy   159 MetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly------------- 173
          :::||||||| ::::|||||||
Db   1087 AATCATACTGTCCACAATATTAATGCTAATGCCGGTATTATGGAAGGTACTGTAAAAGGTAAA---- 1146

Qy   174 LeuGluProLeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsn 193
          ||:::|| ||::: |:::|||||||
Db   1147 TTAAAAGTTTTAAAACAGGATAAAGATACCAAG------------------------------------ 1179

Qy   194 AlaProIleSerAsnProAspGluSerPheLys-----ArgGluSerGluSerAsnLeuVal 212
          |||||||||||:::||| :::|||||||
Db   1180 GCTCCTATAAGCTAAT-----------GTAAAAATTAAAACTTTCTAAAAAGATTGGGATCAGTTAC 1233

Qy   213 SerThrSerGlnLeuSerLeuMetArgGlnAlaLeuGlnLeuIleLeuAspProAsnLeu 232
          :::|||:::|| |||:::|||||||
Db   1234 AAGGACAATCAA----------------AAAGAAATTCAGATTATAACAGACGTACAACGGT 1278

Qy   233 AlaThrLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluSerGlu 252
          ||:::||||||| |||:::|||||||
Db   1279 ...

Db 13795 ATTGGCTATGGTGGAGGATTTAGGTGCTGGTAGCTATGAATTAGATGAATTAGATGAACTGGTAGTGCAACGGA 13854
              |||:::
Qy   506 nLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPhe------------------ThrAspSe 521

Db 13855 TGGCTATATCGTCAATAAACACAACCCATTTATTTGTTAGTGAAGAAGAATTCAAATGATAA 13914
              |||||||:::
Qy   521 rAlaGluLeuAspLysAspLysLysAspTyrHisGly------Phegly------ 536

Db 13915 ACAACCACTAGATCAGATGAGTTAGAGTTGTAAATTATCAAGCAGAAGTAAATGGGACTGTAAAGT 13974
              |||||||||:::
Qy   537 -AspMetAsnAspSerThrLeuAlaLavalAlaLysIleLeuValGluTyrAlaGlnAspSe 556

Db 13975 CAACGGAGCAAGGTCAAAACCTTAGCGGGTGCAGTTTTTGCAATTTACAATCCGATGAGCA 14034
              ||| |||||
Qy   556 rAsnProProGlnLeuAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSe 576

Db 14035 GAATCAGCGCCCAAGGTTCACCGATAACATTCTTGAATCGTGCCAGGAGAAAAAGTTTCTGA 14094
              ||| |||||
Qy   576 r-- 576

Db 14095 AATAACACGGATAAGACTCGGCGAAATTTACGCTAAAGGGCTAAATGAAGGGCATTACGT 14154
              |||||||||:::
Qy   577 ------------------------LeuIleGlyThrGlnTrpHisProGluAs 586

Db 14155 TTTAGTGGAAACGAAAGCACCAACAGCCTATCCGTTAGCACAACAACGCTACATCCA---- 14209
              |||:::||||||
Qy   586 pLeuValAspAIleIleArgMetGluAspPheLysLysGluValIleProvalThrHisAsnLe 606

Db 14210 ---TTTGATGTAACCGCCCAATTAGGAAAAGAGCAGCCAAATTGCTTTAGCGGATCTTAT 14265
              |||||||:::
Qy   606 uThrLeuArgGlyThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGl 626

Db 14266 CAATTATCAAGGAACTGCT------------------------------------CA 14286
              ||| |||||
Qy   626 ------------------------AsnLeuLysHisGlyGl 644

Db 14287 ATTAACCAAAAGAAAAACAGGTGAACGTATCGTTTTGTGGAGACACAAGCAAGGCAA 14346
              |||||||||:::
Qy   644 pLysThrAsnLeuGluPheLysAspGlyLysAlaThrIle----LysThrAs 663

Db 14347 TGAAACAGGG---CAAACCGTAGATGGACAAAACCAATCTGATGTCTAAAATAACTGTTGATAATACGAGAGAAC 14403
              |||:::|||||||
Qy   663 uSerLeuThrLeuGlnGlyLeuProGluGlyTyr------------------ 674

Db 14404 AGTCATGTGGAAAAACTTAGCACCGGGACGTATCGTTTTGTGGAGACACAAGCGCCAAC 14463
              ||| |||||
Qy   675 -SerTyrLeuValLysGluThrAspGlyIleGlyGlyTyrLys-------------- 687

Db 14464 TAGCTATCTTCTTAATGAAACGCCAAGCTTACCGTATTGCCAAAGACAACCAAGG 14523
              |||:::||||||
Qy   687 ------------------------------------AAA------ 687

Db 14524 CAAACCAGCCACTGTGGTACTTAAAGCACCTTTATTAATTACCAAGGTGTGCCAAGCT 14583
              |||||||:::
Qy   687 ------------------------------------ 687

Db 14584 GGTGAAAATTGATCAGACAAAAGAATGCCTTAGCAGGTGCTGAATTTAGCAGAGATGC 14643
              ||| |||||
Qy   688 -ValLysValAsnSerGlnGlyValAlaLeuAsnAla--------------- 698

Db 14644 AGAGACAGGGCAAAACTGTCGCTCGTTCATTACGTGACAACCAAGGGTTAGTTCAAGT 14703
              |||:::|||||||
Qy   699 ------ThrValSerLysThrGlyIleThrSerAspGluThrThrLeuAlaPheGl 714

Db 14704 GAACCACTTACACACCAGGAAAAATATACCTTTGTGGAAACAAAAGCACCGGATGGTTAC 14761
              |||:::|||||||
Qy   714 uAsnAsnLysGluProValValAspThrGlyValAspGlnIleLysIle--AsnGlyTyr 732

```
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (301) 309-8504
    TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 164:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 27360 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
    SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-070-927A-164

Alignment Scores:
    Pred. No.:
    Score:                      149.00
    Percent Similarity:         32.02%
    Best Local Similarity:      19.26%
    Query Match:                3.78%
    DB:                         10

US-09-494-297-2 (1-757) x US-09-070-927A-164 (1-27360)

                            Length:         27360
                            Matches:          181
                            Conservative:     120
                            Mismatches:       320
                            Indels:           320
                            Gaps:              45
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Qy   19 LeuSerLysAsnSerLysArgPheThrValThrLeuValGlyValPheLeuMetIlePhe 38
          |||        ::|||                          |||:::
Db 12224 CTGAAGAAAAACAGCCATGGATGAGACGAACTAATTTACCAGGCCCCATTTCAAAATTTGG 12283

Qy   39 AlaLeuValThrSerMetVal------------------------------GlyAlaLysThr 49
          |||                                                |||
Db 12284 GACCAAGCTAAAAACACAAGTCCTACGGTGAAGGTACAGTAGAGTCCACCGGGGTTATCACA 12343

Qy   50 ValPheGly----------------------LeuValGluSerThrProAsnAlaIle 62
          |||                           |||::::
Db 12344 TTTGGTGGGTGGCCACAAGGGCAATACATTTCGGTGGGACAAAAGCACA------------ 12394

Qy   63 AsnProAspSerSerSerGluTyrArgTrpTyrGlyTyrGlySerTyrValArgGlyHis 82
          |||                                          |||
Db 12395 -------------------------GAAGGCTATACAGTTTCGGAC 12415

Qy   83 ProTyrTyrIleLysGlnPheArgValAlaHisAspLeuValGluGlySerArg 102
          |||                                      ||||||:::  |||
Db 12416 GAATTAGCTAAAGGCCGAGTCATTACTATTAGTGAAGAAAACTTCAGCGGAGAGCACAA 12475

Qy  103 SerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSer 122
          ||||||                  |||  ||||||::         |||
Db 12476 CCA----ACCATTATTAAAAACGATGTCAATAAGTATTTTAGAAAAAAATGGATGAGAAG 12532

Qy  123 ValLysLysTrp--------TyrLysLysHisAspGlyIleSerThrLysPhe--- 137
          |||||||          ::|||
Db 12533 GGTAAAAAGTTAGTCAATGCTCGGCTTTAAATTAGAGCGTACCACGCCGTTACT 12592

Qy  138 ------GluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeu 155
          -----|||:::        |||
Db 12593 CATTGGGAAGAAGTTCCCTTCCGCCCGGATCGAACC-- 12628

Qy  156 ArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlu------Gly 173
          |||                                        ::|
Db 12629 -----AACGCGAATGGCCAGTTGAGAGGTGGATAGT 12658

Qy  174 LeuGluPro---LeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAsp 192
          |||:::|||  :||||                                 |||
Db 12659 TTAAAACCAGGGCTTTATCAGTTCACAGAAAATCGAAGCACCAGCTATCTTTAGAC 12718

Qy  193 AsnAlaPro--------------------------------------------------- 195
          |||
Db 12719 ACGACCCCAAAACGADTTCATCCGTTGACACAAATACGAGGGACAAAATTCGTGDAGTGTCAT 12778

Qy  196 --------------------------IleSerAsnProAspGluSerPheLysArgGluSerAsn 210
                                    |||        :::
Db 12779 GTCAAAAATGCTTAATTACCAAGGTTCTGCTGAACTAATTAAAAAAAGACCAAGCAGGCAAT 12838
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Qy  211 LeuValSerThrSerGlnLeuSerLeuMet----------------ArgGlnAlaLeuLysGln--- 226
          |||                                          ||||||::::
Db 12839 CCATTAGCAGGTGCCAGTTTTCAGTCCTTGACACCACAGACAAGCAGCAGAAACAC 12898

Qy  227 ---LeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPheGln 245
             :::|||                          ||||||
Db 12899 TTAGTTCGGATGAAAACGGAAAAGTCACAGTGACGGAGATTAGCCCCAGAAAATATCAA 12958

Qy  246 LeuSerIlePheGluSerGluAspLysGlyValAspLysLysTyrAsnLysGlyTyrGlnAsnLeu 265
          |||                                      |||||||  :::
Db 12959 TTT---------------GTGGAAACCAAAAGCGCCA 12979

Qy  266 LeuSerGlyGlyLeuValProThrProThrLysProProThrProAspProProMetProPro 285
          ::|||                          |||:::  ||||||:::
Db 12980 ---GCAGGGTACCTTTTAAACACTGAACCAAGTGGCTTTCACGATTGCCAGCAAGCCGATCGG 13036

Qy  286 AsnGlnProGlnThr------------------------------------------ThrSerVal 293
          :::|||                                                 |||:::
Db 13037 GGCAAACCAGCCACAGTTATADGCAACAGGGCTTAACTTTGTTGTAACTATCAAGGCCTAAA 13096

Qy  294 LeuSerAspGlyThrAlaIleGlyAspTyrSerLysLeuLeuGlyLysAlaThrLeuGln 313
          |||                                                  :::
Db 13097 TTAATCAAAAAAGATGTGAATGGA---------CACTTATTAAGGTAGGTCGGACATTTAA 13147

Qy  314 LeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGly 333
          |||                                      :::|||:::::
Db 13148 GTGCTTGATCGGAAGGGAGGGAGAAACGAGTTTCAGTCCTTG--ACGACAAATAAATCAAGG 13204

Qy  334 GluArgIle--------GluLeuSerAspGlyThrThrTyrThrLeuThrGluLeuAsnSerPro 351
          |||                                          |||
Db 13205 GAAATTGTTGCAGAGCCACTTAGCCCCAGAAAATATCGCTTTGTGRAGAAACCAACAAGCGCCA 13264

Qy  352 AlaGlyTyrSerIle----AlaGluProIleThrPheLysVal------GluAlaGly 367
          |||:::        |||::                               |||
Db 13265 ACAGGCTATTATTTAAATACCACGCCGTCCCATTGAAATTGCTGAGAAAAATGCTGGT 13324

Qy  368 Lys------------------------------------------------ValTyrThrIle 372
          |||                                               :::
Db 13325 AAACCACGGGTCGTGGGTTGCTAGTGACAACTTTGTGAGTTACAAAGGGGGCTTTCCAAATC 13384

Qy  373 IleAspGlyLysGlnIleLeuGluAsnPro------------------------------ 381
          |||
Db 13385 GTGAAAACGAAATACGCGACAACCACCATTAGCACGGTGCTGCGTGTTTTGAATTATATGATCAC 13444

Qy  382 AsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluLeuPheSer 401
          |||                                      ||:::
Db 13445 AATAAACA ATCATTAGGATTACAGC---AACGAGTGGCAAAGATGG--- 13488

Qy  402 ValLeuThrThrGlyIleAsnTyr-------------AlaLysPhe-TyrThrTyrAlaLysAs 416
          |||                    |||:::  ||||||:
Db 13489 ---------------CAAAATTATCTTTAGAGACTTGGGCGCCAGGTACCTATTTATTACAAAGA 13536

Qy  416 n-------------------------------------LysAsnGlySerSerGlnValValValTyrCys--- 426
          |||                                                  :::::|||
Db 13537 AATCAAAAGACCACAAAAAATTACCAGATGGCCGAGATATATTATTATCCGAATTAGTAAA 13596

Qy  427 ------PheAsnAlaAspLeuLysSerProAsnSerGluAspGlyGlyLysThrMe 444
          -----|||                                  ||||||
Db 13597 AGTAGAAAATCGTGGGTGCATTCAAAGGTGGATCCGGAGAATT-- 13636

Qy  444 tThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyAsnArgAspLeuPh 464
          |||                                      ||||||::::
Db 13637 -----TTTCCAATTAGG----GCCTTCGCCAATTCAAAGGAACGACGGCGTCTT 13680

Qy  464 eLysTyrThrValLysProArgAspThrAsnProAspThrPheLeuLysHisIleIleLysLy 484
          |||                                      :::      |||
Db 13681 TAAGAAAAATTGAGTGCCAATGCCAAGCCCACTTCCAGGAACGCAGATTTTTAAAAGTGTATCGA-- 13738

Qy  484 sValIleGluLysGlyTyrArg-------------------------GlyLysGlyVal 496
          |||                                          |||::
Db 13739 ----ATCGAAAACGGGGAAAAAATCTTTGAAAGAGAAGGTAACTGCTGAAAAAGATGGTTC 13794

Qy  496 aIle------------------------GluTyrSerGlyLeuThrGluThrGl 506
          |||                         |||
Db 13794 ...
```

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Qy    347 ------------------------GluLeuAsnSerProAlaGly------------TyrSerIleAlaGluProIle 360
                                                            |||                  |||::::
Db   3424 AGTGAATGGCCATAAAATTGATTGTGTCCAAATTAACCCTTATAAAAGCACTATCCGTCCAGTG 3483

Qy    361 ThrPheLysValGlyLeuAlaGlyLysValLysTyrThrIle---IleAspGlyLysGlnIleGlu 379
                        ||||||                    :::            :::|||||||||
Db   3484 ATATATAAA------------TCCCGCCTGTATCTGCTTGGTTGGAACAAAAGGAGATCACC 3534

Qy    380 AsnProAsnLysGlyIleValGluProTyrSerValGluAlaThrTyrAsnAspPheGlu--- 398
                        :::              |||                  ::::|||
Db   3535 AAACAGAACAGGAAATAGTAAAGATAGTGGCTATCAAACTGAAACGGATAATCGTTATGAACTA 3594

Qy    398 --- 398
          |||
Db   3595 AAATTGGCGGCAATACCGCTATGGAATACGGCCAAATCACCTTTGATGTGCAAT 3654

Qy    399 ---GluPheSerValLeuThrThrGlnAsn------ 411
                        |||                  |||
Db   3655 AAAAAAATATCCGAGCTAAAACTGGAAAAAAAATAGAGCGCCCGGACTCTAATTGTGCCGGT 3714

Qy    412 TyrTyrIleAlaLysAsn--- 416
          :::
Db   3715 TATCAAGGTGCAAGATACGTTGCTGGTGAGTGTTTTATAAGCAACAACACACTAGATAGT 3774

Qy    417 ---LysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435
             ||||||      |||                  ||||||      |||||
Db   3775 TATAAAAACGCTTCAAATGCAAGGACTATATATCTTT---GCTGATATGGCATCC------ 3825

Qy    436 AspSerGluAspGlyGlyLysThrMetThrPro--- 446
          |||            |||||||||
Db   3826 AAAGATATGACCCCACAGCAGAACAGCAATGTTTACGGGATAAT 3867

Qy    446 --- 446
Db   3868 AGCTATCAACACAATTTGATACCAATAATGTCAGAGAGAAGTGAATAACCGCTATGCAGAGGAT 3927

Qy    447 ---AspPheThrThrGlyGluValLysTyr 455
             |||::|                :::
Db   3928 TATGAGATTCCTTCCTCGGTAAGTAGCCGTAAAGACTATGGTTGGGGAGATTATTACCCTC 3987

Qy    456 ThrHisIleAlaGlyTyrArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475
                        |||:::            :::|||              ::|||
Db   3988 AGCATGGTATATACGGAGATATCTCCAACTATCAATTACAAAGCCGCCACATACGTTGATTTA 4047

Qy    476 AspThrPheLeuLysHisHisLysThrLysValIleGluGlyLysGlyTyr--- 491
          :::            :::|||||                          ---Arg 491
Db   4048 AAAAATCTATATCTCACCAAAATTTAAGAATTATCATAATGGATATGGAAGGACAGAAGCGC 4107

Qy    492 GluLysGlyGlnAlaIleLeuGluTyrSerGlyLeuThrGlnThrGlnLeuArgAlaAlaThr 511
             :::                  |||      :::
Db   4108 AATCAAATCGCAAATCTGATGAATAAAATATGGCAAACTCAGGTGGTGATAAATTTATTGTTT 4167

Qy    512 GlnLeuAlaIleThrTyrTyrPheThrAspSerAlaGluLeuAspLysSerLeuLysAsp 531
             :::::|||            |||::|
Db   4168 AGCTTGGGGGGTCAATCCAAATAAAACTCGTCAAATAAGCTCATGTTTTACCCCGTCTATCAA 4227

Qy    532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaLeuAlaLeuLeuValGlu 551
          :::::|||            |||            :::::|||
Db   4228 TATAGCGGA------AACACCAGTGGACTCAATCAAGGAGACTACTA 4269

Qy    552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspPheIleProAsnAsn 571
             :::      |||            ::|||
Db   4270 TTCCACCGTGACACCACTTATCCA------TCTAAAGTAGAAGCTTGGATTCCTGGAGCA 4323

Qy    572 AsnLys------ 582
          :::
Db   4324 AAACGTTCTCTAACCAACCAAAAATGCCGCCATTGGGTGATGATTATGCTACAGACTCTCTG 4383

Qy    583 ---HisProGluAspLeuValAspIleLeuArgMetGluSerGluValIle--- 600
             |||            :::::|||            :::
Db   4384 AATAAAACCGGATGATCTTAAGCAACATATATCTTTATGACTCACAGTGAAAAGGGACTCCTACT 4443

Qy    601 ------ProValThrHisAsnLeuThrLeu------ 613
                        |||      :::
Db   4444 GATGTCTCAGGCGCCCAGGACCTAGGAGATTAATACTGCAATTTCTCCAGCAAAAGTTCAGATAATA 4503

Qy    614 GlyLeuAlaGlyLysAspArgThrLysAspPheHisPheGlu------ 626
          |||||||            :::::                  |||
Db   4504 GTCAAAGCGGGTGGCAAGGAGCAAAACTTTTACCGGCAGATAAAGATGTGCTCCATTCAGCCA 4563

Qy    627 ---IleGluLeuLysAsnAsnLys 633
             :::            ::|||||
Db   4564 TCACCTAGCTTGGTGATGAAATGAATTATCAAATTTAATGCCCTTGAAATTAGACGGTTCTGGT 4623

Qy    634 GlnGluGluLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652
             :::            |||            :::|||            :::|||
Db   4624 CTGAATTTTATTAACAACTCAGCCAGTATTGATGTTACTTTTACCGCATTTCGGAGGAT 4683

Qy    653 GlyLys---------------------AlaThrIleAsnLeuLysHisGly 662
          :::                              :::|||
Db   4684 GGCCGCAAACTGGGTTATGAAAGTTTCAGTATTCCTGTTACCGTTAGTACCGGAT 4743

Qy    663 GluSerLeuThrLeuGlnGlyLeuProGluGlyLysTyrSerIleTyrLeuValLysValGluThrAsp 682
          :::::|||||||                        |||::|            |||::|
Db   4744 AATGCCCTGACCCTGCACCATAATGAAAAATGGTGCGCAATATATG------CAA 4791

Qy    683 SerGluGlyTyrLysValLysValAsnSer---------------GlnGlyLeuValAlaAlaAsnAla 698
             :::::|||||::            :::|||            :::
Db   4792 TGGCAATCCTATCGTACCGGCTGAATACTCTATTTGCCGCCGCCGGCGGCC 4851

Qy    699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluLeuAsnAsnLysGlu 718
          |||::|            |||||||||            :::|||            :::|||
Db   4852 ACC------------ACCGGAATCGGATACAATTCTGAGTATGGAAAACTCAGAAATTCAGAA 4902

Qy    719 ProValProThrGlyLysValAspGlnLysIleAsnGlyTyrLeuAlaLeuLeuIleValIle 738
             |||            :::::|||            |||::|            |||||||||
Db   4903 CCG------------CAGTTAGGCAAAGGTTTCTATGCTGTACGTTTCGTGGTGATA 4941

Qy    739 AlaGlyTyrIleSerLeuGlyIleIleTrpGly 747
          :::|||            :::|||
Db   4942 CCTCCCTATACCTATCAAACTCATGGT 4968
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Qy    683  SerGluGlyTyrLysValLysValAsnSer------------------GlnGluValAlaAsnAla  698
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Db   4792  TGGCAATCCTATCGTACCCGCCCTGAATACTCTATTGCCGCGCCAGTTGGTTGCACGCGCC  4851

Qy    699  ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu  718
           |||        ||||||||||        ::::::  :::|||       :::|||
Db   4852  ACC--------ACCGGAATCGATACAATTCTGAGTATGGAAAACTCAGAATATTCAGGAA  4902

Qy    719  ProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIle  738
           |||                    |||::|                  |||  ||||||
Db   4903  CCG--------------------CAGTTAGGCGAAAAGGTTTCTATGCTACGTTCGTGATA  4941

Qy    739  AlaGlyIleSerLeuGlyIleIleTrpGly  747
           :::|||
Db   4942  CCTCCCTATAACCTATCAACTCATGGT  4968
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RESULT 6
US-10-242-056-46
; Sequence 46, Application US/10242056
; Publication No. US20030113323A1
GENERAL INFORMATION:

APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: ffrench-Constant, Richard
APPLICANT: Orr, Gregory L
APPLICANT: Merlo, Donald J
APPLICANT: Roberts, Jean L
APPLICANT: Rocheleau, Thomas A
TITLE OF INVENTION: Insecticidal Protein Toxins from
    Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: DowElanco
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10,242,056
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7551 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-10-242-056-46

Alignment Scores:

Pred. No.:	0.000435	Length: 7551
Score:	152.00	Matches: 148
Percent Similarity:	33.13%	Conservative: 120
Best Local Similarity:	18.29%	Mismatches: 287
Query Match:	3.85%	Indels: 254
DB:	14	Gaps: 37

US-09-494-297-2 (1-757) x US-10-242-056-46 (1-7551)

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Qy    157  AlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluPro  176
           |||       |||                                  |||||||||
Db   2650  GCACAACAAATTGAATCGTCGCCCCACAGGGCGGTTCCGCTTTGGTC---GGGCTGGATTAT  2706

Qy    177  LeuAsnAlaIleLeuArgValThrGlnGlu--AlaValTrpTyrTyrSerAsp----------  192
           :::                     ||     |||       |||   :::
Db   2707  ATTCAATCAATGAAAGAGACACCGACCTATGCCCAGTGGGAAAACGCGGCCAGGGGTATTA  2766

Qy    193  ----------AsnAlaProIleSerAsnProAspGluSerPhePheLysArgGluSerGlu  208
                     :::||           ::::||
Db   2767  ACCGGCGGGGTTGAATTCACAACAGGCTAATACATTACACGCTTTCTGGGATGAATCTCGC  2826

Qy    209  SerAsnLeuValSerThr-------------SerGlnLeuSerLeuMetArgGlnAlaLeuLys  225
           |||       |||                  |||::|:::         |||:::||
Db   2827  AGTGCCGGCATTAAGCACCTACTATATCCGTCAAGTCGCCAAGGCAGCGGGGGCTATTAAA  2886

Qy    226  Gln--------------------------LeuIleAspProAsnLeuAla----------  233
           |||                          |||||||||
Db   2887  AGCCCTGATCGACTTGTATCAAATACTTACTGATTGATAAATCAGGTTTCTCGGCAATAAA  2946

Qy    234  ---ThrLysMetProLysGlnIleValProAspAspPheGlnLeu--------------  246
              ||||||||||||                ||| :::
Db   2947  ACCACCGGAATCGCCGAAGCCATTGCC---AGTATTCAACTGTACGTCAACCGGCCATTG  3003

Qy    247  --SerIlePheGluSerGluAspLysGly-----------------------  255
             ||                        |||
Db   3004  GAAAATGTGGAAGAAAAATGCCAATTCGGGGGTTATCAGCCCCAATTCTTTATCGACTGG  3063

Qy    256  AspLysTyrAsnLysGlyTyrGlnAsnLeuLeuLeuSerGlyLeuValProThrLysPro  275
           ||||||||||||||||||  |||               |||
Db   3064  GACAAATACAATAAAACGCTACAGCACTTGGGCGGTGTTTCTCAATTAGTTTACTACCCG  3123

Qy    276  ProThrProGlyAspProMetProProAsnGlnProGlnThrThrSerValLeuIle  295
           ||| |||         |||      :::                  |||:::
Db   3124  GAAAACTATATTGATCCGACCATGCCTATCGGACAAAACCAAAATGATGGACGCATTACTG  3183

Qy    296  ArgLysTyrAla--------------------------------------  299
           |||::|
Db   3184  CAATCCGTCAGCCAAAGCCAATTAAACGCCGATACCGTCGGAGAGATGCCTTTAGTCTTAT  3243

Qy    300  IleGlyAspTyrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnVal  319
           :::              |||||||||                  ||||||
Db   3244  CTGACATCGTTTGAACAAGTGGCTAATCTTAAAGTTATTAGGCGACATTATCACGAAATATT  3303

Qy    320  AsnSerPheGlnAlaArgValPhe-----------SerSerAsnAspIleGlyGlu---  334
           ||||:::|||  |||            ::::        |||||||||
Db   3304  AATAACGATACAAGGCTGACCTATTTATCGGACTCAGTGAAACTGAATGCCGTGAATAT  3363

Qy    335  -----------------------ArgIleGluLeuSerAspGlyThrTyrThrLeuThr-----  346
                                  :::         ||:::|||
Db   3364  TATTCGGCGCAGTGTCGATCACAGTAAATTCAACGACGGTAAATTCGCGGTAAATCCCTGG  3423
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Db  2650 GCACAACAATTGAATGTCGCCCACAGGGGGCGTTTCCGCTTTGGGTC----GGGCTGGATTAT 2706

Qy   177 LeuAsnAlaIleArgValThrGlnGlu----AlaValTrpTyrTyrSerAsp--------- 192
              :::                    :::
Db  2707 ATTTCAATCAATGAAAGAGACACCGACCTATCCCCAGTGGGAAAACCCGGCAAGGCCGTATTA 2766

Qy   193 --------AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGlu 208
                  :::::::                ::::::
Db  2767 ACCGGCCGGGTTGAATTCACAAACAGGCTAATACATTACACGCTTTTCTGGATGAATCTCGC 2826

Qy   209 SerAsnLeuValSerThr------SerGlnLeuSerLeuMetArgGlnAlaLeuLys 225
              :::::::              ::::::
Db  2827 AGTGCCGCATTAAGCACCTACTATATCCGTCAAGTCACGGGGGGCGGGCTAATTAAA 2886

Qy   226 Gln-----------------------LeuIleAspProAsnLeuAla--------- 233
                                    :::
Db  2887 AGCCCTGATGACTTGTATCAATACTTACTTGATTGATAATCAGTTTCTGGGCAATAAAA 2946

Qy   234 ---ThrLysMetProLysGlnValProAspAspAspPheGlnLeu------ 246
           |||:::::::::        |||||||
Db  2947 ACCACCCGGATCGCCCGAAGCCCATTGCC---AGTAATTCAACTGTACGTCAACCGGGCCATTG 3003

Qy   247 ---SerIlePheGluSerGluAspLysGlyGly---------- 255
              :::::::
Db  3004 GAAAAATGTTGGAAGAAAAATGCCAATTCGGGGGTTATCGACGGCCCAATTCTTTATCGACTGG 3063

Qy   256 AspLysTyrArgAsnLysGlyTyrGlnAsnLeuLeuSerGlyLysValProThrLysPro 275
           |||||||||||||||||||
Db  3064 GACAAATACAGAATAAACGCTACAGCACTTGGGCGGGTGTTTCTCAATTAGTTTACTACCCG 3123

Qy   276 ProThrProGlyAspProMetProProAsnGlnProThrThrSerValLeuIle 295
           |||||||              :::
Db  3124 GAAAACTATATATTGATCCGACCAATGCCATTGCGTTATCGGACAAAATGTACGGACCATTACTG 3183

Qy   296 ArgLysTyrAla------------- 299
           :::
Db  3184 CAATCCGTCAGCCAAAGCCAAATTAAAACGCCGATACCGTCGAAGAGATCCCTTTATGTCTTAT 3243

Qy   300 IleGlyAspTyrSerLysLeuLeuGlyValAlaThrLeuGlnLeuGlyLysAspAsnVal 319
                    :::                :::
Db  3244 CTGACATCGTTTGAACAAGTGGCTAATCTTAAAGTTATTAGCGCACATATCACAGATAATATT 3303

Qy   320 AsnSerPheGlnAlaAargValPhe------------SerSerAsnAspIleGlyGlu--- 334
           :::::::   |||                |||||||
Db  3304 AATAACGATCAAGGCGCTGACCTATTTTATCGGACTCAGTGAAACTGATGCCGGTGAATAT 3363

Qy   335 ----ArgIleGluLeuSerAspGlyThrThrLeuThr------ 346
                   :::::::
Db  3364 TATTGGCGCAGTGTCGATCACAGTAAAATCAACGACGTAAAATTCGGCGTAATGCCTGG 3423

Qy   347 ------GluLeuAsnSerProAlaGly-----TyrSerIleAlaGluProIle 360
                 :::::::              |||
Db  3424 AGTGAATGGCCATAAAAATTGATTGTCCAATTAAACCCTTATAAAAGCACTATCCGTCCAGTG 3483

Qy   361 ThrPheLysValGluAlaGlyLysValThrThrIle---IleAspGlyLysGlnIleGlu 379
                |||:::                |||:::|||
Db  3484 ATATATAAA------TCCGCCTGTATCTATCTGCTCTGGTTGGAACAAAAGGAGATCACC 3534

Qy   380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrArgAsnPheGlu--- 398
                   |||               |||              :::::::
Db  3535 AAACAGCAGGAGAAAATAGTAAAGAATGGCTATCAAACTGAAAACGGATTATCGTTATGAACTA 3594

Qy   398 ------------GluLeuAsnSerGlnThrValLysThrAspLysAsnLeuGluPhe---- 411
                       :::
Db  3595 AAATTGGCGGCCATATCCGCTATGATGGCACTTGGAATAACGGCCAATACACCTTTGATGTCGT 3654

Qy   399 --GluPheSerValLeuThrThrGlnAsn----------------- 411
             |||:::                   :::
Db  3655 AAAAAAAATATCCGAGCTAAAAACTGAAAAAAAATAGAGCGCCCGGACTCTATTGTGTCCGGT 3714

Qy   412 TyrTyrTyrAlaLysAsn----------- 416
           |||:::
Db  3715 TATCAAGGTGAAGAATACGTTGCTGGTGATGTTTTATAACCAACAGAACACACTAGATAGT 3774
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Qy   417 --LysAsnGlyTyrSerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435
             ||||||              ||||||:::          |||||||:::
Db  3775 TATAAAAACGGCTTCAAGTCCAAGGACTATATATCTTT--GCTGATAGGCATCC------- 3825

Qy   436 AspSerGluAspGlyGlyGlyLysThrMetThrPro------------ 446
           |||              ||||||
Db  3826 --------AAAGATAATGACCCCAGAAGAACAGAGCAATGTTTATCGGGATAAT 3867

Qy   446 ------------AspPheThrThrGlyGluValLysTyr 455
                       |||:::
Db  3868 AGCTATCAACAATTGATACCAATTAATGTCAGAAGAGTGAATAACCGCTATGGCAGGGAT 3927

Qy   455 AspPheThrThrGlyGluValLysTyr 455
           |||:::
Db  3928 TATGAGATTCCTTCCTCGGTAAGTAGCCGTAAAGACTATGGTTGGGGAGGATTATTACCTC 3987

Qy   456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475
              :::          ||||||              |||
Db  3988 AGCATGGTATATAACGGAGATAATTCCAACTACTATCAATTACAAGCCGGATCAAGTGATTTA 4047

Qy   476 AspThrPheLeuLysHisHisIleLeuValIleGluLeuValSerGlyTyr---------- 491
                             ::::::              |||
Db  4048 AAAATCTATATCTCACCAAAATTAAGAACGATTAATGGATAAGGACAGAAGGGC 4107

Qy   492 GluLysGlyGlnAlaIleGluGlyTyrSerGlyLeuGluThrGlnLeuLeuArgAlaAlaThr 511
                    ||||||              :::          |||
Db  4108 AATCAACGCAAATCTGATGAATATAAAATATGGCAAACTAGGTGATGAAAAATTTAATTGTTTAT 4167

Qy   512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaLeuAspLeuLeuHisLysLeuLysAsp 531
                    :::          ||||||              |||
Db  4168 AGCTTGGGGTCAATCCAAATAAACTCGTCAAATAAGCCTACGTTTATACCCGTCTCATCAA 4227

Qy   532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuValAlaAlaLysIleLeuValGlu 551
           :::          |||              :::
Db  4228 TATAGCGGA----------AACACCAGTGGACTCAATCAAAGGGAGACTACTA------ 4269

Qy   552 TyrAlaGlyIleAspSerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsn 571
                 :::          |||||||          :::
Db  4270 TTCCACCGTGACACCACTTATCCA------TCTAAAGTAGAAGCTTGGAATTCCTGGAGCA 4323

Qy   572 AsnLys------------TyrGlnSerLeuLeuIleGlyThrGlnTrp---------- 582
           |||||||              |||
Db  4324 AAACGTTCTCTAACCACCAAAAATGCCGCCATCTGGGTGATTAATGGCTTACAGACTCTCTG 4383

Qy   583 ---HisProGluAspSerLeuValAspIleLeuArgMetGluAspLysLysGlyValIle-- 600
              |||||||          :::              |||
Db  4384 AATAAACCGGATCATCTTAAGCAATATATCTTTATGACAGTAAAGGGACACTGCTACT 4443

Qy   601 ------ProValThrHisAsnLeuThrLeu------ArgLysThrValThr 613
                 :::          |||              :::
Db  4444 GATGTCTCAGGCCCAGTAGAGATTAATACTGCAAATTTCTCCAGCAAAAAGTTCAGATAATA 4503

Qy   614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu----------- 626
              :::          |||||||
Db  4504 GTCAAACGCGGGTGGCAAGGAGCAAAACTTTTACCGGCAGAAGATGTCTCCAATTCAGCCA 4563

Qy   627 ------------IleGluLeuLysAsnAsnLys 633
                       :::
Db  4564 TCACCTAGCTTTGATGAAAATGAATTATCAATTAATGCCCTTGAAATAGAACGGTTCGGT 4623

Qy   634 GlnIleGluLeuGluSerGlnThrValLysThrAspLysAsnLeuGluPhe--LysAsp 652
              :::          ||||||              |||
Db  4624 CTGAATTTTATTAACAACTCACGCGTATTGATGTTACTTTTGATGTCAGAGGAT 4683

Qy   653 GlyLys------------AlaThrIleAlaSerLeuLysHisGly 662
           ||||||              :::
Db  4684 GCCGCAAAACTGGGTTATGAAAAGTTTCAGTATTCCCTCAAGGTTAAGTACCGGAT 4743

Qy   663 GluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAsp 682
              |||||||||||||                   :::
Db  4744 AATGCCCTGACCCTGCACCCATAATGAAAAATGGTGCGCAAATATATG------CAA 4791
```

```
RESULT 5
US-09-817-514A-1

Sequence 1, Application US/09817514A
Patent No. US2002007847BA1

GENERAL INFORMATION:
  APPLICANT: ffrench-Constant, Richard
  APPLICANT: Bowen, David
  APPLICANT: Rocheleau, Thomas
  APPLICANT: Waterfield, Nicholas
  TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
  FILE REFERENCE: 61645
  CURRENT APPLICATION NUMBER: US/09/817,514A
  CURRENT FILING DATE: 2000-03-26
  PRIOR APPLICATION NUMBER: US 60/191806
  PRIOR FILING DATE: 2000-03-24
  NUMBER OF SEQ ID NOS: 8
  SOFTWARE: Patentin version 3.0
  SEQ ID NO 1
    LENGTH: 7551
    TYPE: DNA
    ORGANISM: Photorhabdus luminescens

US-09-817-514A-1

Alignment Scores:
  Pred. No.:              0.000435
  Score:                  152.00
  Percent Similarity:     33.13%      Length:         7551
  Percent Identity:       18.29%      Matches:         148
  Best Local Similarity:              Conservative:    120
  Query Match:            3.85%       Mismatches:      287
                                      Indels:          254
                                      Gaps:             37

US-09-494-297-2 (1-757) x US-09-817-514A-1 (1-7551)
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Db  2995 ACGACTGAC------------------------GACAACGGCAAGCTGACAATTCGGCAATATTCGC 3036
                ||||||                       :::||||||::::||:::|||    |||:::::
Qy   661 HisGlyGluSerLeuThrLeuGln---GlyLeuProGlyGlyThrTyrSerTyrLeuValLys 679
              ::::|||                      ||:::||||||:::|||:::|||    :::
Db  3037 TATGGCACTTACATTTAAAAGAAATCAAGGCGCGCCTGACGGATAATACG------ATCAGC 3090
         |||||                       ||||::::||||||::::|||::::||||||
Qy   680 GluThrAspSerGluGlyThrTyrLysValLysValAsnSerGln------------- 693
              :::|||                      ||||::::||||||::::||||||
Db  3091 GACGCCTATGCAGACGGGGTGTCTCCGTTGAGATTAACACAGATAACAAGACAGAA 3150

Qy   694 ------GluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu 709
                |||   |||       |||       ||||||
Db  3151 CTTTACAAAGTCGTGAATGACAAGAAGAGAAATAAGGTGACGGCTTATCAAACAACAAGACGAA 3204

RESULT 4
US-10-242-056-48
Sequence 48, Application US20030113323A1
Publication No. US20030113323A1
GENERAL INFORMATION:

APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: ffrench-Constant, Richard
APPLICANT: Orr, Gregory L
APPLICANT: Merlo, Donald J
APPLICANT: Roberts, Jean L
APPLICANT: Rocheleau, Thomas A
TITLE OF INVENTION: Insecticidal Protein Toxins from
TITLE OF INVENTION: Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: DowElanco
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/242,056
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/242,056
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
```

```
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO:   48:
SEQUENCE CHARACTERISTICS:
LENGTH: 5547 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-10-242-056-48
DB:

Alignment Scores:
Pred. No.:                              .
Score:                 152.00          Length:          5547
Percent Similarity:    33.138          Matches:         148
Best Local Similarity: 18.298          Conservative:    120
Query Match:           3.858           Mismatches:      287
DB:                    14               Indels:         254
                                        Gaps:           37

US-09-494-297-2 (1-757) x US-10-242-056-48 (1-5547)

Qy   157 AlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluPro 176
              |||       |||||||       |||:::||||||   |||:::|||
Db  2386 GCACAACAAATTGAATGTTGCGCCCCACACAGGGCGGTTCCGCCTTTGGTC---GGGCTGGATTAT 2442

Qy   177 LeuAsnAlaIleAlaArgValThrGlnGlu---AlaValTrpTyrTyrSerAsp--- 192
              :::||||||       |||       |||   |||:::|||
Db  2443 ATTCAATCAATGAAAAGAGACAACCGACCTATGCCCAGTGGGAAAACGGCGCAGGCGTATTA 2502

Qy   193 ------AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGlu 208
                |||       |||::::|||       |||:::|||
Db  2503 ACCGCCGGGTTGAAATTCACACAACAGGGGTTAAATACATTACACGCTTTTTGGATGAAATTCGC 2562

Qy   209 SerAsnLeuValSerThr------SerGlnLeuSerLeuMetArgGlnAlaLeuLys 225
              :::||||||       |||   |||:::|||
Db  2563 AGTGCCGCCATTAAGCACCTACTATATCCGTCAAGTCGCCAAGGCACGCGGGCTATTAAA 2622

Qy   226 Gln----------------LeuIleAspProAsnLeuAla---------------- 233
                |||:::|||||||
Db  2623 AGCCGTGATGACTTGTATCAATAACTTACTGATTGATAATCAGGTTTCTGCGGCAATAAAA 2682

Qy   234 ---ThrLysMetProLysGlnValProAspAspPhePheGlnLeu--------- 246
              |||||||       |||::::|||
Db  2683 ACCACCCGGATCGCCCGAAGCCCATTGCC---AGTATTCAAACTGTACGTCAACGGGCCATTG 2739

Qy   247 ---SerIlePheGluSerGluAspLysSGly-------------------- 255
              :::|||       |||:::|||
Db  2740 GAAAAATGTGGAAGAAAAATGCCAATTCGGGGTTATCAGCCCGCCAATTCTTTATCGGACTGG 2799

Qy   256 AspLysTyrAsnLeuSerGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysPro 275
              |||||||||||||||       |||:::|||
Db  2800 GACAAATACAATAAACCCTACAGCACTTGGGCGGGGTGTTTCTCAATTAGTTTACTACCCG 2859

Qy   276 ProThrProGlyAspProMetProProAsnGlnProGlnThrThrSerValLeuIle 295
              |||       |||:::|||
Db  2860 GAAAACTATATTGATCCGACCATGCCTATCGGACAAACCAAAAATGATGGACGACCATTACTG 2919

Qy   296 ArgLysTyrAla---------------------- 299
              |||::::|||
Db  2920 CAATCCGTCAGCCAAAGCCAATTAAACGCCGATACCGTCGAAGATGCCGTTTATGTCTTAT 2979

Qy   300 IleGlyAspTyrSerLysLeuLeuGluGlyValAlaThrLeuGlnLeuThrGlyAspAsnVal 319
              :::|||||||       |||:::|||
Db  2980 CTGACATCGTTTGAACAAGTGGCTAATCTTAAAGTTATTAGGCGAATAACAGAATAATAATT 3039

Qy   320 AsnSerPheGlnAlaArgValPhe----------- 334
              ||||||       |||       |||
Db  3040 AATAACGATCAAGGGCTGACCTTATTTTTATCGGACTCAGTGAAAACTGATGCCGTGAATAT 3099

Qy   335 -----------------ArgIleGluLeuSerAspGlyThrTyrThrLeuThr----- 346
              :::||||||       |||
Db  3100 TATTGGCGCAGTGTCGATCACAGTAAATTCAACGACGGTAAAATTCGCGGCGTAAATGCCTGG 3159

Qy   347 ------------GluLeuAsnSerProAlaGly-----TyrSerIleAlaGluProIle 360
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Qy  114 AlaPheProLeuGlySerAspSerSerValLysLysTrpTyrLysLysHisAspGlyIle 133
            |||     |||:::||                       :::::||||||:|||
Db  985 GCTTACCGCTCATCATGTGACGGACTACCCGCAAAAACCGAACGAAAGGGGA 1044

Qy  134 SerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluAsnGln 153
            |||:                                  :::
Db 1045 AACGGTCCATTTAGGAACAAGGCA 1068

Qy  154 LysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlyGly 173
            |||                                         :::
Db 1069 ------------------------------ACGTTCGGCGGA 1086

Qy  174 LeuGluProLeuAsnAla-- 184
            ||||                   :::
Db 1087 CTGGAACCGGCGTTCTGCGAGAGCCCT------------ 1086

Qy  185 GluAlaValTrpTyrTyrSerAspSerAspAsnAlaProIleSer------- 199
            :::                  |||||||                  AsnPro
Db 1147 TCGTCGACAGGTTATAAAAGCCATTCACAGACGGTTCACTGGACGACGA 1206

Qy  200 AspGluSerPheLysArgGluSerGluSerAsnLeuVal------------ 216
            :::        |||||||                       SerThrSerGln
Db 1207 GGAGAGAAAAAATCGACGAATCCAAAGCGAGCGATTAACAGACTCCGT 1266

Qy  217 LeuSerLeuMetArgGlnAlaIleLeuLysGlnLeu------- 233
            :::                                    IleAspProAsnLeuAla
Db 1267 TTGCATCTTGTTCAGATTCCTTAAAGGTGATTCCGATTACTT 1326

Qy  234 ThrLys--------------MetProLysGlnValProAspAspPheGlnLeuSer--- 247
            :::                 |||:||                        LeuIleArgLys
Db 1327 GAGCAGGCTGGAACGCCTCAACGGAGGCAAGGAATTATACGGCTTCTCTGAT 1386

Qy  248 ------------IlePheGluSerGluAspLysGlyLeuGlyLysAlaThrLysTyrAsn 264
                        |||                                 :::
Db 1387 GGGTTTGAAATCAAATTTAACCAAGATGTTACCGGGAGAGAAA 1446

Qy  265 LeuLeuSerGlyLysGlyLeuValProThrLysProProThrProGlyTyrAspProMet--- 283
            |||                                              :::
Db 1447 GAGGTCAACACGGGCGTAATCATCGATAAATCAACACCTATACGA 1506

Qy  284 ------------ProProAsnGlnProGlnThrThrSerVal---------- 297
                                   :::                       LeuIleArgLys
Db 1507 GGAACAGGAGAATCAAAGAAAGCTTCAGGTACAGCCGTTACAGGA 1566

Qy  298 TyrAlaIleGlyAspThrTyrSerLysLeuLeuGluGlyValAlaThrThrLeuGlnLeuThrGlyAsp 317
            |||                                              :::
Db 1567 TACTCCAAACATTGATTACAAGGAGAGAAAACGGTCGGAT 1617

Qy  318 AsnValAsnSerPheGlnLeuAArgValPheSerSerAsnAspGlyGluArg----- 335
            |||:                                        :::
Db 1618 AACAAAAAACTACACGATGAAACAATTGGAAGTTGGATGACAAATTT 1677

Qy  336 IleGluLeuSerAspGlyThrThrPheThrGluLeuAsnSerProAlaGlyTyrTyrSer 355
            |||                                         :::
Db 1678 CTCACGCTCCTGACGGATCAATTCCCGCCTTCAGGTAGTGACGAAT 1722

Qy  356 IleAlaGluProIleThrPheLysValGluAlaGlyLysValAlaGlyValThrTyrThrIleIle----- 373
            :::                                              :::
Db 1723 --------AACAAAAACGCTGAAGAAGGCAAAGAC 1767

Qy  374 ----------AspGlyLysGlnIleGlu--- 384
                       :::                   AsnProAsnLysGlu
Db 1768 CCGGATCATGAAGGTTTCTCTGGAACTCACG 1827

Qy  385 IleValGluProTyrSerValGluIleThrTyrAsnAspPheGluGlyPheSerValLeuThr 404
            |||:                                        :::
Db 1828 CTTAAGATCACGTAATACCACGAATATGAAGCCGACTTTTTCCAACG 1887

Qy  405 ThrGlnAsnTyrAlaLysPheTyrTyrAla--------------LysAsnLysAsnGlySer 420
            |||                                        :::
Db 1888 ACGGCAGAAATCAACGTGGACTCACGACGACCACTGAACGCAAAAATAAG 1947
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Qy  421 Ser--- 421
            |||
Db 1948 AGTTTTTACGGCGGAATCGCCAGACAATCCCACAACGGCTTCAAACACGG 2007

Qy  422 ------------GlnValValTyrCysPheAsnAlaAspLeuLysSerProAspSerGlu 438
                        :::                                  :::
Db 2008 GTTTCAAAAGAAATCACGTGGAAAAATCGGCATCAACTATAATGGAGAGC 2067

Qy  439 AspGlyGlyLysThrMetThrProAsp--------PheThrThrGlyGluVal----- 453
            |||                                    |||
Db 2068 CCTTATATTAAAAGATTCTTTAGCAGACGACCAGCAATTTGAAAAAGGCTCGG 2127

Qy  454 ---------LysTyrThrHisIleAlaGlyLeuAspLeuPhe----- 464
                          ||||                       :::
Db 2128 AAGAGCTATTCAGTTAATAAAGACGGTTCCATCACACAGAAGG 2187

Qy  465 LysTyrThrVal--LysProArgAspThrProAspThrPheLeuLysSerHisIleLys 483
            :::||||                                  :::
Db 2188 CAAATGATGTGGAAGAGCCGTCGGCCTGCCAATAAACAAACTTTGAC 2247

Qy  484 Lys--------------ValIleGluLeuGlyTyrArgGluLysGlnAlaIle 497
            |||                                  |||||||
Db 2248 ACGGACGAATTCCGTCCCGTATCTTATTGAATTTAAAAACATC 2307

Qy  498 GluTyr-------------SerGlyLeuThrGluThrGln 506
            :::                                  |||
Db 2308 AAGCACGATCCTTACACCAATAAGGCACCGGATTATTC 2367

Qy  507 LeuArgAlaAlaThrGlnLeuAlaThrGlnLeuAlaIleIleGluTyrTyrPheThrAspSerAlaGluLeuAspLys 526
            |||                                        :::
Db 2368 TTGACGGCCATCCGTTCCGTTCGGTCGCA------- 2412

Qy  527 AspLysLeuLysAspTyrHisIleGlyPheGlyAsp--------- 542
            |||                                  MetAsnAspSerThr
Db 2413 AAAGGAGGCAAACAAAACGGAGGTTATGTCGATCAATGCAAT 2472

Qy  543 LeuAlaValAlaLysIleLeuValGlyTyrAlaGlnAspSerAsnProProGlnLeuThr 562
            |||                                        |||
Db 2473 TCGGTGTTGGAAGATGTAAAAGTCACCGATACTCCGGATACCAAT 2526

Qy  563 AspLeuAspPhePhe--- 567
            |||                LysTyrGlnSerLeuIle
Db 2527 GCTGAAGATTCTTTAAAGTTTATCAGGCTGAAATATGATGAAAAAGG 2586

Qy  567 ------- 567
                               :::
Db 2587 AGCAGCGGAAAACTTTGTCCCGGATGAGTGTTCAGCTTAAGAAAGGCG 2646

Qy  568 ---IleProAsnAsnAsn----- 572
            :::
Db 2647 GATATCAAGACCGACAATGCAACCGCGGACAATCATTGTCCTGAAATTTACAGGCGAT 2706

Qy  573 ----------LysTyrGlnSerLeuIle--- 579
                                   |||        Gly
Db 2707 TACAAAAAAATCGACCGGCGCCTATGTTGTTATTCAAATATCAATAATTGCCGGC 2766

Qy  580 ThrGlnTrpHisProGluAspLeuValAspIleIle--- 592
            |||                                  Arg
Db 2767 ACGAGCGGCGCCATGTTAACAAAGTGTCGATTCGGGGACGAATGTCCAGGAACAGACC 2826

Qy  593 MetGluAspLysLysGlyLysValIleProValThrHis-- 604
            :::                                  |||
Db 2827 CAGGAAAAACAACAGCTCCGGTCTTTGTTGCCGGTTCAGCTCAGGG 2886

Qy  605 ------AsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyLysAspArgThrLys 621
            :::||||                                  :::
Db 2887 GAAAGAGGAAGAGCCTGACAATCCTTAAA----ACGGGAGAAGACGGACGCCGCTTTCC 2940

Qy  622 AspPheHisPheGluIleLeuGluLysAsnAsnLysGluLeuLeuSerGlnThrVal 641
            |||                                        :::
Db 2941 GGACCAGATTTTCAATTGCGGACAAAAAGATAATGAGCAG-----CTCCTGCGCACAGGA 2994

Qy  642 LysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIle--AsnLeuLys 660
            |||                                        :::
Db                                                              — 
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Qy    297 LysThrTyrAlaIleGlyAspTyrSerLysLeu-------LeuGluGlyValAlaThrLeuGln 313
                  :::||| |||  |||||
Db  10396 CGTTACATTATT-----GAGTATAAAAACGCCAATGGCTGACGTGCCAAACTCTTTAT 10452.

Qy    314 LeuThrGly---------AspAsnValAsnSerPheGlnAlaArgValPhe 327
              |||        |||||||||
Db  10453 ATAACAGGGACAGCGGAAAGAAGAACCAATCGAATAATAATGAAGGCTCTGCTTCGGTTTCT 10512

Qy    328 SerSerAsnAspIleGlyValArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347
                       |||
Db  10513 GTTCAAAAT-------GAAGCGTTAGACATTTTGAGTGCAACA 10548

Qy    348 LeuAsnSerProAlaGlyTyrSerIleAlaGlyPheLysProIleThrPheLysValGluAlaGly 367
                 :::                 |||
Db  10549 ------CAAGCGCGGAATCCAACATTAAAAATGTAACAAACG 10587

Qy    368 LysValTyrThr-------IleIleAspGlyLys------GlnIleGluAsnProAsnLysGlu 384
              |||    |||      :::||||||||||||||
Db  10588 ACAGTAACAACAAAAAATATTGATAATAAACACATCACAACGATTGAA 10647

Qy    385 IleValGluProTyrSerValGlnAlaTyrAsnAspPheGluGlyPheSerValLeuThr 404
                                :::                      |||
Db  10648 TTAACACCAAAAGGCACAACCAATGCTCAAATCGATTTGAATTCTATTACCGTG------ 10701

Qy    405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysSerSerGlyValVal 424
                            |||
Db  10702 ------AAAGGCGTGCCAGAAGAATGCT 10722

Qy    425 TyrCysPheAsnAlaAspLeuLysSerProAspSerGluAspGlyGlyLysThrMet 444
              :::  |||                    |||:::|||||||||
Db  10723 TAT--------TCATTAGAGAAGACTACAAACAGGTGCGAAAGTCATT 10761

Qy    445 ThrProAspPheThrArgThrGlyGlu----------ValLysTyrThrHisIleAlaGlyArg 461
              ||:::|||         ||      :::||||||||
Db  10762 TTTAAAGACTATACAGTTGACAGAAAACATTACGATTGAATACAATACGGTCTCTGCAAAC 10821

Qy    462 AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481
                          ||||||           |||::::::
Db  10822 GCTGGCCAAATCTATACAGAAAACAACAATCGACTCTGAAACATTGAACCAGATGTCTGCT 10881

Qy    482 IleLeuLysLysValIle-------GluLys 488
                          :::               ::
Db  10882 AGCAAGAAAAAAGTCACACTGCCCAATCACACATTGAAATTCTCAGAAGGTGATGCGGAA 10941

Qy    489 GlyTyrArgGluLysGlyGlnAlaIleGluLysTyrSerGlyLeuThrGlnThrGlnLeuArg 508
              |||                    |||:::  :::
Db  10942 GGTATTGTTTATTTAGCAACTGCCACATTCTACACGCATAACGTAGAGGATGAAAACCAA 11001

Qy    509 AlaAlaThrGlnLeuLeuAlaIleThrTyrTyrPheThrThrAsp----------SerAlaGluLeu 524
              |||                  :::              ::     |||
Db  11002 GCAATTGGCGGAAGGTTTCTTTGACTAATTGATAATGTCACGCATACAGCAACGGAATTT 11061

Qy    525 AspLysAspLysAspTyrHisGlyPheGlyTyrAspMet------AsnAspSerThrLeu 543
              |||                               |||
Db  11062 ACAACAGATGAAAAAGGTCAATACTCCTTTGATCCATGACGAGGTGATTATACTTTG 11121

Qy    544 AlaValAlaLysIleLeuValGluTyrAlaGlnAsnAspSerAsnProProGlnLeuThr--- 562
              |||||||:::  ||||||::          :::            |||||||
Db  11122 CGAGTAACGAAGTGACCCGCCAGGAATATTCCGGGATGAAGAG------TATTTGACAGGA 11175

Qy    563 ----------AspLeuAspPhePheIlePro---------- 569
                        |||||||
Db  11176 AAAGCCATTAAGCTGGGTCAAAGGAGACAACCAACTAAAAAATTCCATTAACGAAAAACAATT 11235

Qy    570 AsnAsnAsnLysTyrGln---------SerLeuIleGlyThrGlnTrpHisPro 584
                                |||      :::
Db  11236 GATCACAGTCGTTTTACAAGATTTAGTCGGCGATTCATGAGAAACCA 11295

Qy    585 GluAspLeuValAspIleIleArgMetGluAspGlyLysLys---GluValIleProValThr 603
              |||||||      |||:::                  |||||||
Db  11296 GAAGAG------AACTTGTTTCAGCAACAAGATCAAGACGTTCCCTTCGAA 11349


Qy    604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuValAlaGlyLysAspPhe 623
                      ||||||:::|||::|||
Db  11350 ------AAAATCACTGTTTCAGGTCAACTTGATAACASCAAAGCAGGCGTT 11394

Qy    624 HisPheGluIleLeuGluLeuLysAsnAsnLysGlnIleGluLeuAsnSerGlnThrValLysThr 643
              :::                  ||||||||||:::|||
Db  11395 TATCCAATTATTTACAGTGACGAAGGTAAAGAAGAGAAACAGCCTATGTGACGGTCAAACC 11454

Qy    644 AspLysThrAsnLeuGluPheLysLysAspGlyLysLysAlaThrIleAsnLeuLysHisGlyGlu 663
              |||:::::                  ||||||         :::
Db  11455 GACCAAATCTAAGTTAGGATGGTCAAAGAT------GGTGAT 11502

Qy    664 SerLeuThrLeuGlnGlyLeuProGlyLeuGlyTyrSerTyrLeuValLysGluThrLysSer 683
              |||                      ::|||
Db  11503 TCGTTGGAAA------CCAGA------GATAATTTCGTTCGGCCGACAGACAGACAAA 11544

Qy    684 GluGlyTyrLysVal----------LysValAsnGlnGluValAlaAlaAsnAlaThrVal 700
              |||:::         |||||||:::|||
Db  11545 ACAGGTCAAGACGTTCCGTTGAAAAAAATTGATGTTCAGGGAACAGTGAAT------GTT 11598

Qy    701 SerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsn 715
              :::         |||            :::::|||
Db  11599 GATAAAATAGGC----------GATTATGAAATTGTCTATAAAAAT 11634
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RESULT 3
US-09-974-300-2632
Sequence 2632, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
   APPLICANT: Berka, Randy M.
   APPLICANT: Clausen, Ib Groth
   TITLE OF INVENTION: Methods For Monitoring Multiple Gene
   TITLE OF INVENTION: Expression
   FILE REFERENCE: 10085.500-US
   CURRENT APPLICATION NUMBER: US/09/974,300
   CURRENT FILING DATE: 2001-10-05
   PRIOR APPLICATION NUMBER: 09/680,598
   PRIOR FILING DATE: 2000-10-06
   PRIOR APPLICATION NUMBER: 60/279,526
   PRIOR FILING DATE: 2001-03-27
   NUMBER OF SEQ ID NOS: 8481
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 2632
   LENGTH: 4557
   TYPE: DNA
   ORGANISM: Bacillus licheniformis
US-09-974-300-2632

Alignment Scores:
Pred. No.:
Score: 8.37e-05   Length: 4557
Percent Similarity: 156.00   Matches: 175
Best Local Similarity: 34.05%   Conservative: 124
Query Match: 19.93%   Mismatches: 297
DB: 3.95%   Indels: 283
                         10   Gaps: 43

US-09-494-297-2 (1-757) x US-09-974-300-2632 (1-4557)

```
Qy     54 ValGluSerSerThrProAsnAlaIleAsnProAspSerSerGluTyrArgTrpTyr 73
              :::::::::|||||||||::|||||||   :::|||
Db    752 ATAAAGCATCAACCCCGGCAGGTCATGACACTGCACCTCAACAAAAATTGGATC 811

Qy     74 ----------GlyTyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
                        |||                      :::|||
Db    812 AGGTGAAAAAATGCCAAGCTGCGAGACAGTTTCCAGAGGGGCTG-ACC-- 867

Qy     89 ArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSer---------- 103
              ::|||   :::::|||||||::::::              |||
Db    868 AAAGTT---TATCACGCTGGATGTCAACATAGTAGTGGTTCAGCGCCGGGAGGAAGTT 924

Qy    104 ----------TyrGlnVal----------TyrCysPheAsnLeuLysLys 113
                        |||             :::
Db    925 CTTTCAGGCTACACCCGTAGACGCCAGATGGAAAGTCACATTCGACGGTGAGATAGAGTTCG 984
```

INFORMATION FOR SEQ ID NO: 242:

    TELEFAX: (301) 309-8512
    TELEPHONE: (301) 309-8504
    TELECOMMUNICATION INFORMATION:
    REFERENCE/DOCKET NUMBER: PB369
    REGISTRATION NUMBER: 40,302
    NAME: Kenley K. Hoover
ATTORNEY/AGENT INFORMATION:

    FILING DATE: 1997-11-14
    APPLICATION NUMBER: 60/066,009
    FILING DATE: 1997-05-06
    APPLICATION NUMBER: 60/044,031
    FILING DATE: 1997-05-16
    APPLICATION NUMBER: 60/046,655
PRIOR APPLICATION DATA:

    CLASSIFICATION: <Unknown>
    FILING DATE: 04-May-2000
    APPLICATION NUMBER: US/09/070,927A
CURRENT APPLICATION DATA:

    SOFTWARE: ASCII Text
    OPERATING SYSTEM: MSDOS version 6.2
    COMPUTER: HP Vectra 486/33
    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER READABLE FORM:

    ZIP: 20850
    COUNTRY: USA
    STATE: Maryland
    CITY: Rockville
    STREET: 9410 Key West Avenue
    ADDRESSEE: Human Genome Sciences, Inc.
CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 982
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

        Steven Barash
        Patrick J. Dillon
    APPLICANT: Charles A. Kunsch
GENERAL INFORMATION:

  Patent No. US20020120116A1
  Sequence 242, Application US/09070927A
US-09-070-927A-242

RESULT 2

Alignment Scores:
Pred. No.:

	Length:	12445
Score: 161.00	Matches:	159
Percent Similarity: 34.83%	Conservative:	104
Best Local Similarity: 21.06%	Mismatches:	326
Query Match: 4.08%	Indels:	166
DB: 10	Gaps:	40

US-09-494-297-2 (1-757) x US-09-070-927A-242 (1-12445)

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CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 60/046,655
  FILING DATE: 1997-05-16
  APPLICATION NUMBER: 60/044,031
  FILING DATE: 1997-05-06
  APPLICATION NUMBER: 60/066,009
  FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
  NAME: Kenley K. Hoover
  REGISTRATION NUMBER: 40,302
  REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (301) 309-8504
  TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
  LENGTH: 15614 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-070-927A-45

Alignment Scores:
Pred. No.:
Score:                        5.91e-08
Percent Similarity:           196.00
Best Local Similarity:        35.57%
Query Match:                  23.11%
DB:                           4.97%
                              10
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US-09-070-927A-45 (1-15614)                Length:      15614
                                            Matches:     165
                                            Conservative: 89
                                            Mismatches:  245
                                            Indels:      216
                                            Gaps:        41
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US-09-494-297-2 (1-757) x US-09-070-927A-45 (1-15614)

Qy    88 PheArgValAlaHisAspLeuArgValAsnLeuGluGlySer--------ArgSerTyrGln 105
         ||||||                                               ||  :::
Db  9047 TTCAGGTTCAAAACATTA-CCAGAAGTGTCGCTAACAGGCCCTACACAATTAATAGTAATGAG 9105

Qy   106 ValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLys 125
         |||||                                    ||||||||||||||::||||
Db  9106 ATTTAT-----------------------------TTGGGTAAAGGGCAAGAAATTCAAAATT 9138

Qy   126 TrpTyrTyrLysHisAspGlyIleSerThrLysPheGluAsp------------ 139
         ||| ||||                               ||  :::
Db  9139 CATTATCAAGTACGT----------ATTCAAACAGAGTCAGAAAAACTTCAAACCTGATTTTTGG 9192

Qy   140 TyrAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
         ||||                                               |||
Db  9193 TATCAAAATGAAATGGTCGGACAACGTTTCAGCCACTGGCCCCTGAAAAAAGTTGAT 9252

Qy   160 TyrAsnGlyHisProGlnAsnAlaAsnGlyIleLeuGlyLeuGluProLeuAsnAla 179
         ::|                                               |||
Db  9253 TTT----------------GGGGTTCCTTCGGAAAAAGCACCT-----GGC 9282

Qy   180 IleArgValThrGlnGluAlaValIleTrpTyrTyrSerArgAsnAlaProIleSerAsnPro 199
         :|||::::                               |||     |||
Db  9283 GTGAAGTTAAACGTGAAAAAAATCTGGGAAGAGTATGAGTTGGAGCGCGCAAGTCGGCCA 9342

Qy   200 AspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSer----------- 215
         |||                                           :::
Db  9343 GATAATGTGATTTATGAAAATTAGTAGAAAGCAAGTAACTGACACAGCCAACTGCCAAACT 9402

Qy   216 ------GlnLeuSerLeuMetArgGlnAlaLeuLysGlnIleLeuIleAspProAsnLeu 232
         |||||||                                           :::
Db  9403 GGGTATAATTAAATTATCAAAACAGAAAAATGATACCAGCAATAGTTGGGAGCGCGCAAAAAT 9462

Qy   233 AlaThrLysMetProLysGlnValProAspProAspPheGln------LeuSerIlePheGlu 250
         ||:::::                              |||     ||: 
Db  9463 GTAACCCAACTTTCCAAAACCGCGGATGAAAGCTATACAAGAAGTTCTTGGGCTTCCCACAA 9522

Qy   251 SerGluAspLeuLysGlyAlaSpLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu 270
         :::|||||||                              ||:::
Db  9523 TACAACAATCAAGGACAAGCAAGCTTTCAAT----------TATCAAACAACCGTGAATTAGCA--- 9573
```

```
Qy   271 ValProThrLysProThrProGlyIleAspProProMetProProAsnGlnProGlnThr 290
         ||||||                                    |||       |||
Db  9574 GTTCCTGGTTACAGTCAGTGCAAGAAAAAATCGACAGATACTACTTGGAAAAACAAGCAGTTC 9633

Qy   291 ThrSerVal------------LeuIleArgLysTyrAlaIleGlyLysAspTyrSerLysLeu 307
         ||                  ||:::::                              |||
Db  9634 AAGCCATTAGAATTTAAAAGTAATCAAAAATTCTTCCTCAGGTGAG-----------AAAAACTTA 9687

Qy   308 GluGlyValAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPhe 327
         |||                                        ||:
Db  9688 GTGGGACCCGTCTTTTGAAATTGAGTTGGTAAAAATGTT-------CAAACAACATATTGTG 9738

Qy   328 SerSerAsnAsp-----------------IleGlyGluArgIleGluGluSerAspGly--Thr 342
         :::                        |||                              |||
Db  9739 GACAATAAAAGATTGGGTAGCTATTCCTTGCCAAAAGAAGATGTGCGCCTACAAAAAGGGGGAACGC 9798

Qy   343 TyrThrLeuThrGluLeuAsnSerProAlaGlyTyrTyrSerIleAlaGluProIleThrPhe 362
         |||||||||||||||::                         :::
Db  9799 TATACATTAACTGAAGTAAAAAGCACCTGCCAGGACACATGAGTTAGGCAGAAAAACGACTTGG 9858

Qy   363 LysValGluAla------------GlyLysValTyrThrIleIleLeuGluGlyLysGlnIleGlu 379
         ||||                   ::|||||                              |||
Db  9859 CAAATTGAGGTGAGTGAGCAAGGCAAAGTA------AGCATCGGATGGCAACGAAAGTGACC 9912

Qy   380 AsnLysAsnGlySerSer-GlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 399
         |||                ::|||::::
Db  9913 ACCACAAAATCAAGTTATT----------CCATTGGAAATGAA-----AATAAATTTTCTCT 9960

Qy   400 PheSerVal-----------LeuThrThrGlnAsnTyrAlaLysPheThrTyrTyrAlaLys 415
         :::                ||:::                              |||
Db  9961 TTGCCAATCAGAATTAGAAAATTACACCATGCAAAAT----------GGCAAA 10002

Qy   416 AsnLysAsnGlySerSer-GlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435
         |||                ::|::::
Db 10003 CAAGTGAACTTAGCAGAGGCGACTTTTGCGTTGCAAGAA-----------AATAAATTTTACT--- 10042

Qy   435 oAspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysTy 455
         |||                              |||       :::
Db 10043 AAAATGCTGCAAGGACGAAGTTACCAAAACTGTGGGACAACTCAAAA 10083

Qy   455 rThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPr 475
         |||                              |||
Db 10084 AACAGATAACTACAGGATTGAAGATTGAGCTATTTT------------------ 10111

Qy   475 oAspThrPheLeuLysHisIleLysLysValIleGluGluLysGly---TyrArgGluLysG1 494
         |||                              |||  ||
Db 10112 ------------------AAAATTAGTAGAACCTGGTGAGTATCGA--- 10138

Qy   494 yGlnAlaIleGluTyrSerGlyLeuThrGlnLeuArgAlaAlaThrGlnLeuLeuAl 514
         |||                              |||
Db 10139 ---ATGGTGGAACAATCAGGA------------------CCATTAGGCTACGACACTCTTGCTGG 10182

Qy   514 aileTyrThrTyrPheThrAspSerProAlaGluLeuAspLysAspLysAspTyrHisG1 534
         |||                              |||
Db 10183 AAATTATGAAATTTACT------------GTTGATAAA--- 10207

Qy   534 yPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGl 554
         |||                              |||
Db 10208 -TATGGGAAA----------------ATTCACTATGCAGG 10230

Qy   554 n--------AspSerAsnProGlnLeuThrAspLeuAspPhePheIleProAsnAs 571
         |||                              |||::::
Db 10231 CAAAAAATTGAAGAAAAATGCGCCAGAAATGGACA---------------------- 10264

Qy   571 nAsnLysTyrGlnSerLeuIleGlyThrGlnTrpHisProGluAspIleI1 591
         |||                              |||
Db 10265 ---------------------------------CTGACACATCAAAATAATTTGAAACCTTT 10293
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Qy   591 eArgMetGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArgLys-- 610
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 19, 2003, 17:28:10 ; Search time 459 Seconds
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Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Database : Published_Applications_NA:*

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0494297_@CGN_1_1_252_@runat_13082003_122948_28206
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB Length	DB ID	Description
1	196	5.0	15614	10	US-09-070-927A-45	Sequence 45, Appl

ALIGNMENTS

2	161	4.1	12445	10	US-09-070-927A-242	Sequence 242, App
3	156	4.0	4557	10	US-09-974-300-2632	Sequence 2632, Ap
4	152	3.9	5547	14	US-10-242-056-48	Sequence 48, Appl
5	152	3.9	7551	9	US-09-817-514A-1	Sequence 1, Appl
6	152	3.9	7551	14	US-10-242-056-46	Sequence 46, Appl
7	149	3.8	27360	10	US-09-070-927A-164	Sequence 164, App
8	148	3.8	3827	10	US-09-870-759-44	Sequence 44, Appl
9	147	3.7	4047	9	US-09-815-242-4843	Sequence 4843, Ap
10	147	3.7	4050	9	US-09-815-242-9039	Sequence 9039, Ap
11	146.5	3.7	2522	9	US-09-842-552-98	Sequence 98, Appl
12	144.5	3.7	7035	9	US-09-815-242-8615	Sequence 8615, Ap
13	139.5	3.5	3504	9	US-09-070-927A-167	Sequence 167, App
14	139	3.5	7101	14	US-10-011-366-9	Sequence 9, Appl
15	139	3.5	19031	10	US-09-070-927A-89	Sequence 89, Appl
16	137.5	3.5	20072	10	US-09-070-927A-364	Sequence 364, App
17	137	3.5	9509	10	US-09-070-927A-4724	Sequence 4724, Ap
18	136.5	3.5	2523	9	US-09-815-242-8653	Sequence 8653, Ap
19	136.5	3.5	2526	9	US-09-815-242-454	Sequence 454, App
20	136.5	3.5	4358	8	US-08-781-986A-472	Sequence 472, App
21	136.5	3.5	6806	9	US-09-070-927A-4724	Sequence 5, Appl
22	136.5	3.5	14756	14	US-10-160-758-5	Sequence 134, App
23	136.5	3.5	14756	14	US-10-060-036-134	Sequence 338, App
24	135.5	3.4	2661	11	US-09-769-787-338	Sequence 1, Appl
25	135	3.4	3687	10	US-09-117-447-1	Sequence 227, App
26	134.5	3.4	14934	14	US-10-084-817-227	Sequence 144, App
27	133.5	3.4	2616	10	US-09-919-039-144	Sequence 1, Appl
28	133.5	3.4	2412	10	US-09-858-525A-1	Sequence 292, App
29	133.5	3.4	20561	10	US-09-070-927A-292	Sequence 145, App
30	132.5	3.4	2458	11	US-09-919-039-145	Sequence 95, Appl
31	132.5	3.4	2636	13	US-10-002-600-95	Sequence 5, Appl
32	132.5	3.4	2766	10	US-09-117-447-5	Sequence 527, App
33	131.5	3.3	7107	10	US-09-070-927A-527	Sequence 27, Appl
34	131	3.3	6360	12	US-09-769-744A-27	Sequence 7, Appl
35	130.5	3.3	14536	14	US-10-160-758-7	Sequence 339, App
36	129.5	3.3	1998	11	US-09-769-787-339	Sequence 9, Appl
37	129.5	3.3	2520	10	US-09-858-525A-9	Sequence 268, App
38	129.5	3.3	4702	8	US-08-781-986A-268	Sequence 264, App
39	129.5	3.3	5171	8	US-08-781-986A-264	Sequence 62, Appl
40	129.5	3.3	11560	14	US-10-177-293-62	Sequence 168, App
41	128.5	3.3	7963	8	US-08-781-986A-168	Sequence 480, App
42	128	3.2	4226	14	US-10-037-270-480	Sequence 1, Appl
43	128	3.2	4319	11	US-09-839-996-1	Sequence 1, Appl
44	128	3.2	4319	14	US-10-080-505-1	Sequence 3, Appl
45	128	3.2	4896	9	US-09-740-274-3	Sequence 3, Appl